

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:19:36 ; Search time 16 Seconds

(without alignments)
914,482 Million cell updates/sec

Title: US-10-662-431-2

Sequence: 1 MAMMEVGGESLGQTCVLIV.....NEHLIDMDEASFGAFLVG 281

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	1478	100.0	281	TN10_HUMAN	P50591 homo sapien
2	930	62.9	291	TN10_MOUSE	P50592 mus musculu
3	267.5	18.1	318	TN11_RAT	Q96822 r tumor nec
4	258.5	17.5	316	TN11_MOUSE	Q35235 h tumor nec
5	251.5	17.0	317	TN11_HUMAN	O14788 h tumor nec
6	189.5	12.8	279	TN16_MOUSE	P41047 mus musculu
7	187	12.7	280	TN16_CERVO	Q9bdm1 cervocepus
8	186	12.6	281	TN16_HUMAN	Q9p166 homo sapien
9	185	12.5	280	TN16_MACMU	P48023 mus musculu
10	184	12.4	282	TN16_CHICK	Q9p166 macaca mula
11	182	12.3	282	TN16_RAT	Q91848 gallus gall
12	177.5	12.0	278	TN16_PIG	Q9bea8 sus scrofa
13	164	11.1	261	TN15_BOVIN	P316940 rattus norv
14	160	10.8	261	TN15_HUMAN	O95150 homo sapien
15	159.5	10.8	240	TN14_HUMAN	O43557 homo sapien
16	152.5	10.3	239	TN14_MOUSE	Q9qy19 mus musculu
17	152	10.3	261	TN15_MOUSE	Q9bdm3 callithrix
18	150.5	10.2	261	TN15_CAJMA	Q9bdm3 callithrix
19	149.5	10.1	260	TN15_FELCA	Q9bdm3 callithrix
20	148	10.0	261	TN15_MACMU	O97605 felis silve
21	147.5	10.0	260	TN15_MOUSE	Q9bdm3 callithrix
22	147.5	10.0	261	TN15_HUMAN	Q9bdm3 callithrix
23	143	9.7	261	TN15_PIG	P29965 homo sapien
24	140	9.5	260	TN15_MOUSE	Q95m45 sus scrofa
25	136.5	9.2	235	TN15_RABIT	P04924 cryocolagus
26	135	9.1	229	TN15_CEREL	P27548 mus musculu
27	134.5	9.1	204	TN15_PIG	P26445 sus scrofa
28	134	9.1	234	TN15_BOVIN	P59664 bos indicus
29	133.5	9.0	260	TN15_RAT	Q92242 rattus norv
30	133	9.0	232	TN15_PIG	P23563 sus scrofa
31	131.5	8.9	234	TN15_CAVPO	P51435 cavala porce
32	131.5	8.9	233	TN15_BUBBU	P59693 bubalus bub
33	131.5	8.9	233	TN15_PAPSP	P33620 papio sp. (

34	131	8.9	234	1	TN15_HORSE	P29553 equus cabal
35	131	8.9	253	1	TN15_SPAU	O81f43 sparus aura
36	130.5	8.8	233	1	TN15_BOVIN	O06599 bos taurus
37	129.5	8.8	235	1	TN15_PIG	P36938 peromyscus
38	127.5	8.6	204	1	TN15_BOVIN	Q06600 bos taurus
39	127.5	8.6	233	1	TN15_MARMO	Q05734 marmota mon
40	125.5	8.5	233	1	TN15_HUMAN	P01375 homo sapien
41	123.5	8.4	235	1	TN15_MOUSE	P06804 mus musculu
42	123.5	8.4	235	1	TN15_RAT	P16599 rattus norv
43	122	8.3	205	1	TN15_HUMAN	P01374 homo sapien
44	122	8.3	232	1	TN15_PANTR	Q8h2d0 pan troglod
45	122	8.3	234	1	TN15_CAPI	P13296 capra hircu

ALIGNMENTS

RESULT 1
TN10_HUMAN STANDARD; PRT; 281 AA.
AC P50591;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).
GN TNFSF10 OR TRAIL OR APO2L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96111955; PubMed=8777713;
RA Wiley S.R., Schooley K., Smoljak P.J., Din W.S., Huang C.-P.,
RA Nicholl U.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.;
RT "Identification and characterization of a new member of the TNF
RT family that induces apoptosis.";
RL Immunity 3:673-682(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96278649; PubMed=8663110;
RA Plett R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,
RA Ashkenazi A.;
RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor
RT necrosis factor cytokine family.";
RL J. Biol. Chem. 271:12687-12690(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=1247932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,
RA Rana S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McWiley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettmann M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schenker A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[4]
 RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
 RP MEDLINE=20017054; PubMed=10549288;
 RX Hymowitz S.G., Christinger H.W., Fuh G., Utsch M., O'Connell M.,
 RA Kelley R.F., Ashkenazi A., de Vos A.M.;
 RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
 RT complex with death receptor 5.";
 RL Mol. Cell 4:563-571 (1999).
 RN [5]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
 RP PubMed=10542098;
 RX Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
 RA Jones E.Y., Screaton G.R.;
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
 RT specificity in apoptotic initiation.";
 RL Nat. Struct. Biol. 6:1048-1053 (1999).
 RN [6]
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.
 RP MEDLINE=99413670; PubMed=10485660;
 RX Cha S.-S., Kim M.S., Choi Y.H., Sung B.U., Shin N.K., Shin H.C.,
 RA Sung Y.C., Oh B.-H.;
 RT "2.8 A resolution crystal structure of human TRAIL, a cytokine with
 RT selective antitumor activity.";
 RL Immunity 11:253-261 (1999).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 CC possibly also to TNFRSF1B/OPG. Induces apoptosis. Its activity
 CC may be modulated by binding to the decoy receptors
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF1B/OPG that cannot
 CC induce apoptosis.
 CC -1- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
 CC trimer.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
 CC AND PROSTATE.
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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 CC -----
 DR EMBL: U37518; AAC50332.1; -;
 DR EMBL: U57059; AAB01233.1; -;
 DR EMBL: BC032722; AAH32722.1; -;
 DR PDB: 1D0G; 22-OCT-99.
 DR PDB: 1D4Y; 01-NOV-99.
 DR PDB: 1D2Q; 11-FEB-00.
 DR PDB: 1D66; 26-SEP-01.
 DR Genew; HGNC:11925; TNFSF10.
 DR MIM; 603598; -;
 DR GO: GO:0005887; C:integral to plasma membrane; TAS.
 DR GO: GO:0005625; C:soluble fraction; TAS.
 DR GO: GO:0005102; F:receptor binding; TAS.
 DR GO: GO:0007267; P:cell-cell signaling; TAS.
 DR GO: GO:0006917; P:induction of apoptosis; TAS.
 DR GO: GO:0007165; P:signal transduction; TAS.
 DR Interpro: IPRO06052; TNF_family.
 DR Interpro: IPRO08983; TNF_like.
 DR Interpro: IPRO03636; TNF_subf.
 DR Interpro: IPRO0229; TNF_1.
 DR Pfam: PF00229; TNF_1.
 DR Prodom: PD002012; TNF_subf; 1.
 DR SMART; SMO0207; TNF_1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 DR Cytokine; Apoptosis; Transmembrane; Signal-anchor; Metal-binding;
 KM Zinc; 3d-structure.
 KM DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

FT FT (POTENTIAL).
 FT DOMAIN 39 281 EXTRACELLULAR (POTENTIAL).
 FT METAL 230 230 ZINC.
 FT STRAND 123 127
 FT TURN 130 131
 FT TURN 137 139
 FT STRAND 149 150
 FT STRAND 163 165
 FT STRAND 167 170
 FT TURN 171 172
 FT STRAND 173 176
 FT STRAND 180 193
 FT STRAND 205 213
 FT STRAND 220 228
 FT STRAND 237 250
 FT TURN 252 253
 FT STRAND 255 260
 FT STRAND 263 265
 FT STRAND 266 267
 FT TURN 270 272
 FT TURN 274 281
 SQ SEQUENCE 281 AA; 32509 MW; DDAAP78DAAB2P6D CRC64;
 Query Match 100.0%; Score 1478; DB 1; Length 281;
 Best Local Similarity 100.0%; Pred. No. 8e-115;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEYQGGPSIGOTCVLIVIFVLLQSLCAVATYYVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEYQGGPSIGOTCVLIVIFVLLQSLCAVATYYVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DSDYMDPNDSESNNSPCQWQVKQRLQYVRKMLIRISEFTITSTVOEKQONISPLVRRGPQ 120
 DB 61 DSDYMDPNDSESNNSPCQWQVKQRLQYVRKMLIRISEFTITSTVOEKQONISPLVRRGPQ 120
 QY 121 RVAAHITGRGNSNTLSSNSKXKERLGRKINSWESSRGHSLSMLHINRGLVYHEKG 180
 DB 121 RVAAHITGRGNSNTLSSNSKXKERLGRKINSWESSRGHSLSMLHINRGLVYHEKG 180
 QY 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKKSARNSCWSDAEYGLY 240
 DB 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKKSARNSCWSDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 RESULT 2
 ID TN10 MOUSE STANDARD; PRT; 291 AA.
 AC P50532;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
 DE apoptosis inducing ligand) (TRAIL protein).
 GN TNFSF10 OR TRAIL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9611955; PubMed=8777713;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
 RA Micholl V.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
 RA Goodwin R.G.;
 RT "Identification and characterization of a new member of the TNF
 RT family that induces apoptosis.";
 RL Immunity 3:673-682 (1995).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and

FT	STRAND	186	187
FT	TURN	191	192
FT	STRAND	194	196
FT	STRAND	198	201
FT	TURN	202	203
FT	STRAND	204	207
FT	STRAND	211	224
FT	HELIX	225	227
FT	STRAND	234	245

Query Match 17.5%; Score 258.5; DB 1; Length 316;
Best Local Similarity 26.4%; Pred. No. 4.4e-14;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10

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QY      10 PSIGOTCVLIIVIFVLLQSICVAATYYVFTELKQMOKRYSKGIACF-----LIKEDSDY 64
           ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db       43 PAASRSNFMLLGLGLOGVCSIALFLYRAQMD--PKRISEDSHCHYRIILRLHNAGL 100
           ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

QY      65 WDP--NDEBSMNSPCWQVKWOLRQLVRMKILRTISEETISTVOEKQOINTSPL----- 113
           ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db      101 QDSTLESEDTLPDSCRMRKQAFQGAVOK-----ELGHIVGPDRFGAPAMM 146
           ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

QY     114 -----VREKPGQVFA--AHTTGRGKSNTLSPNSKNKEKLGRKINSWESRSGHSPTS 165
           ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
          147 EGSNLDAIDKORCKPACPAPFAHLT-----INAAISIPSGSKVTL---SSMYHDR-GWAKTS 196
           ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

```

Dy		166	NLRINRELNYLTHEGFVYISQTYREOEELIKENTKNDKCWQVYLYKYT-SYPDILLMK	224
Dz		197	NMTLSNGKLARNQGCGFYLVLANICFRHHETSGSVPDYQLGMVVYVKNSIKIPSSHNLMK	256
Ey		225	SARSCMSKAIEYGLYSITYGQIELKENDRIFPVSVTNEHLIMDHDEASFPGALFLV	280
Fy		257	GGSTRKMWSGNSEFFHFSINVGFEFKLRAGEEISIQVSNPSILDEDDOATYFGAFEXV	312
Gy	RESULT 5			
Hx	TN11_HUMAN			
Iy	TN11_HUMAN	STANDARD; PRT; 317 AA.		
Jz	AC	O14723; Q96Q17; G9P2Q3;		
Ky	AD	014788; 014723; Q96Q17; G9P2Q3;		
Lz	DT	16-OCT-2001 (Rel. 40, Created)		
Mz	DT	16-OCT-2001 (Rel. 40, Last sequence update)		
Nz	DT	10-OCT-2003 (Rel. 42, Last annotation update)		
Oz	DE	Tumor necrosis factor ligand superfamily member 11 (Receptor activator		
Pz	DE	of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-		
Qz	DE	induced cytokine) (TRANCE) (osteoprotegerin ligand) (OPGL) (Osteoclast		
Rz	GN	TNFSF11 OR RANKL OR TRANCE OR OPGL.		
Sz	OS	Homo sapiens (Human).		
Tz	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Uz	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
Vz	OX	NCBI_TaxID=9606;		
Wy	RN	[1]		
Xz	RP	SEQUENCE FROM N.A. (ISOFORM 1).		
Yz	RC	TISSUE=Bone marrow, and Peripheral blood;		
Zz	RX	MEDLINE=98032977; PubMed=9367155.		
Aa	RA	Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,		
Ba	RA	Tometsko M.E., Koux E.R., Teepe W.C., DuBoise R.F., Cosman D.,		
Cb	RA	Galibert L;		
Dc	RT	"A homologue of the TNF receptor and its ligand enhance T-cell growth		
Ec	RT	and dendritic-cell function.";		
Fd	RL	Nature 390:175-179(1997).		
Gf	RN	[2]		
Hg	RP	SEQUENCE FROM N.A. (ISOFORM 1).		
Ih	RC	TISSUE=Lymph node;		
Ji	RX	MEDLINE=98227661; PubMed=9568710;		
Kj	RA	Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,		
Lk	RA	Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hu H,"		
Ml	RA	Surigavan J., Hawkins N., Davy E., Capparelli C., Eli A., Delan Y.-X.,		
Nm	RA	Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., O'Leary J.,		
On	RA	Boyle U.J.;		
Pa	RT	"Osteoprotegerin ligand is a cytokine that regulates osteoclast		
Qb	RT	differentiation and activation.";		
Rc	RL	Cell 93:165-176(1998).		

[3]
 RN SEQUENCE FROM N.A. (ISOPFORMS 1; 2 AND 3).
 RP Ikeda T., Kuroyama H., Hirokawa K.,
 RA "Determination of human RANKL isoforms."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 [4]
 RN SEQUENCE OF 73-317 FROM N.A.
 RP TISSUE=thymocytes;
 RA MEDLINE=97460112; PubMed=9312132;
 RX Wong B.R., Rho J., Aron J., Robinson E., Orlinick J., Chao M.,
 RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
 RT Choi Y.;
 RT "RANCE is a novel ligand of the tumor necrosis factor receptor family
 RT that activates c-Jun N-terminal kinase in T cells."
 RL J. Biol. Chem. 272:25190-25194(1997).
 [5]
 RN SEQUENCE FROM N.A. (ISOPFORM 2).
 RP TISSUE=Tongue;
 RA MEDLINE=20175237; PubMed=10708588;
 RX Nagai M., Kyakumoto S., Sato N.;
 RT "Cancer cells responsible for humoral hypercalcemia express mRNA
 RT encoding a secreted form of ODF/RANCE that induces osteoclast
 RT formation."
 RL Biochem. Biophys. Res. Commun. 269:532-536(2000).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF11B/ODG and to
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Augments the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcemia of malignancy.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);
 CC Secreted (isoform 2). A soluble form of isoform 1 arises by
 CC proteolytic processing (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=OI4788-1; Sequence=Displayed;
 CC Name=2; Synonyms=SODF;
 CC IsoId=OI4788-2; Sequence=VSP_006447;
 CC Name=3;
 CC IsoId=OI4788-3; Sequence=VSP_006446;
 CC -1- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT WEAK
 CC IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,
 CC PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
 CC -1- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.
 CC -1- PTM: The soluble form of isoform 1 derives from the membrane form
 CC by proteolytic processing (By similarity). The cleavage may be
 CC catalyzed by ADAM17.
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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 CC -----
 CC EMBL: AF019047; AAB86811.1; -
 CC EMBL: AF053712; AAC39731.1; -
 CC EMBL: AB064269; BAB79694.1; -
 CC EMBL: AB064227; BAB71768.1; -
 CC EMBL: AB064270; BAB79695.1; -
 CC EMBL: AF013171; AAC51762.1; -
 CC EMBL: AB037599; BAA90488.1; -
 CC HSSP: P50591; IDOG.
 CC Genew: HGNC:11926; TNFRSF11.
 CC MIM: 602642;
 CC GO: GO:0005576; C:extracellular; NAS.
 CC GO: GO:0005887; C:integral to plasma membrane; NAS.

DR GO: GO:0005164; F:tumor necrosis factor receptor binding; NAS.
 DR GO: GO:0006555; P:immune response; NAS.
 DR GO: GO:0030316; P:osteoclast differentiation; NAS.
 DR InterPro: IPR006052; TNF_family.
 DR InterPro: IPR008983; TNF_like.
 DR InterPro: IPR003636; TNF_1like.
 DR Pfam: PF00229; TNF_1.
 DR Prodom: PD002012; TNF_subf. 1.
 DR SMART: SM00207; TNF_1.
 DR PROSITE: PS00251; TNF_1; FALSE_NEG.
 DR PROSITE: PS50049; TNF_2; 1.
 DR Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
 KW Signal-anchor; Alternative splicing.
 FT CHAIN 1 317
 FT FT
 FT CHAIN 140 317
 FT FT
 FT DOMAIN 1 47
 FT TRANSMEM 48 68
 FT FT
 FT DOMAIN 69 317
 FT SITE 139 140
 FT CARBOHYD 171 171
 FT CARBOHYD 198 198
 FT VARSPPLIC 1 47
 FT FT
 FT VARSPPLIC 1 73
 FT FT
 FT CONFLICT 194 194 A -> G (TN REF. 4).
 FT SEQ 317 AA; 35478 MW; 766176446348097F CRC64;
 SQ SEQUENCE
 Query Match 17.0%; Score 251.5; DB 1; Length 317;
 Best local Similarity 24.1%; Pred. No. 1.7e-13;
 Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;
 QY 10 PSLGQTCVILIVFTVLGSLCAVTVYFTNLEKQMDKSKSGIACF-----LKED--- 61
 DB 42 PASRSMFVALILGLGQVVCVALFFPRAQMD--PNRISDGHCIYRIILRHNAQF 99
 QY 62 -DSYMPDNDEESNNSPCWQVW-----OLRLVRKMLRFTSEETI-----STVOEKQ 107
 DB 100 QDTTLESQTKLIPDSCKRIKQAFQAVQKELOHIVGSGHIRKAMVDGSMWDLAKRSK 159
 QY 108 QNISPLVRBRGQPVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNL 167
 DB 160 LEAQPE-----AHLT-----INATDIPSGSKVSL-----SSWYHDR-GWAKISNM 199
 QY 168 HLRNGELVTHEKGFYITISQTYFRPOBEIKENTKNDKQWQIYKXT-STPDPILMKSA 226
 DB 200 TFSNGKLIVQDGFYLLYANICFRHHTSGDLATEYLQLVVYTKSIKIPSSHTLMKGG 259
 QY 227 RNSCWKDAVGLGYSIYGIFELKENDRIFVSTNEHLIDMDHEASFQAFVY 280
 DB 260 STYVNSGNSBFHFTYSLNVGGFFTLRSGERISTVNSPLDIPDQATYRFAFVY 313
 RESULT 6
 TNEF_MOUSE
 ID TNEF_MOUSE STANDARD; PRT; 279 AA.
 AC P41047; O61217; Q9R1P7;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
 DE ligand).
 GN TNFRSF6 OR FASL OR APTLIG1 OR GLD.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOPFORM FASL).
 RX MEDLINE=94185175; PubMed=511063;

[illegible]

QY 203 DKOMQYIY-KTYSYDPDILMKASR-NSCWSKAEYGLSYGGIFELKENDRIFYSV 260
 Db 202 NQPLNKHVMRSKRPEDVLMEERKLNCTT--GQIWAHSYSLCAVRLTISADHLVANI 259
 QY 261 TNEHLIDMDHEASFPFAP 278
 Db 260 SGLSLINFESKTFPGLY 277

RESULT 7
 TNF6_CERTO
 ID TNF6_CERTO STANDARD: PRT; 280 AA.
 AC Q9BDN1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
 DE (CD95L protein).
 DE TNFSF6 OR FASL OR CD95L.
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OC NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;
 RX MEDLINE=2138618; PubMed=11491535;
 RA Villinger F., Bostlik P., Mayne A.E., King C.L., Gernain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/FasL ligand and co-stimulatory molecules";
 RT Immunogenetics 53:315-328 (2001).
 RL

- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
 transduces the apoptotic signal into cells. May be involved in
 cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
 CC peripheral tolerance, in the antigen-stimulated suicide of mature
 CC T cells, or both. Binding to the decoy receptor TNFRSF6/DCR3
 CC modulates its effects (By similarity).
 CC - SUBUNIT: Homotrimer (Probable).
 CC - SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
 CC similarity).
 CC - PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC - SIMILARITY: Belongs to the tumor necrosis factor family.

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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF344847; AAK37606.1; -
 CC HSSP: P01375; 4TSV
 DR InterPro: IPR008064; Fas_Ligand.
 DR InterPro: IPR006053; TNF_abc.
 DR InterPro: IPR006052; TNF_family.
 DR InterPro: IPR008983; TNF_1like.
 DR InterPro: IPR003636; TNF_subf.
 DR Pfam: PF00229; TNF_1.
 DR PRINTS: PRO1681; FASTIGAND.
 DR PRINTS: PRO1234; TNECROSISFCT.
 DR ProDom: PD002012; TNF_subf; 1.
 DR SMART: SM00207; TNF_1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PSS0049; TNF_2; 1.
 KM Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
 FT CHAIN 1 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT MEMBER 6, MEMBRANE FORM.
 FT CHAIN 129 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY

FT DOMAIN 1 80 MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
 FT TRANSMEM 81 101 CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT PRO-RICH.
 FT POLY-PRO.
 FT CLEAVAGE (BY SIMILARITY).
 FT DISULFID 201 232 POTENTIAL.
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 280 AA; 31407 MW; 729EA60067BD398 CRC64;

Query Match 12.7%; Score 187; DB 1; Length 280;
 Best Local Similarity 22.1%; Pred. No. 3e-08;
 Matches 61; Conservative 56; Mismatches 91; Indels 68; Gaps 10;

QY 4 MEVGGSPSLGQTCVLIIVFTVLQSLCAVYVYFTNELKQMDKXSGGLACFLKEDDS 63
 Db 70 LKRGNGHSTG-LCLIVMEFMVIALVGLGLGFWLFHQLQKELAF-----LRSTTS 118
 QY 64 YNDPDEBSMNSPCWQVKKQLRQIVRKXMIIRSEPTISTVQKQONISPLVERGPQRYA 123
 Db 119 -----QKTAASLEQIGHPS-PEPKKEQRYV 145

QY 124 AHITGRGRSNTLSSPNSKNEKALGRKINSWESRSGHSFLSNLHRLNGELVTHKERYX 183
 Db 146 AHLTG-----KPNSSMPL-----EWEDT-YGIYLSGAVKKKGLVYNERGLYF 189

QY 184 IYSQYFRPQEBEIKENTKNDKQMOYIY-KTYSYDPDILMKASRNSCWSKAEYGLYNI 242
 Db 190 VYSKYVFRQ-----SCTNLPLSHKVYVRNKKYQDVLVMEGRKWS-YCTTGQWMAHSS 242

QY 243 YQGIFELKENDRIFYSVTNEHIDMDHEASFPFAP 278
 Db 243 YIGAVFNLTSTHLYVWSELVWNEESQTFPGLY 278

RESULT 8
 TNF6_HUMAN
 ID TNF6_HUMAN STANDARD: PRT; 281 AA.
 AC P48023; Q9BZP3;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
 DE (Apoptosis antigen ligand) (APLT) (CD178 antigen).
 GN TNFSF6 OR FASL OR APTLGL.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=95105731; PubMed=7528780;
 RA Alderson M.;
 RT "Fas ligand mediates activation-induced cell death in human T
 RT lymphocytes";
 RL J. Exp. Med. 181:71-77 (1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=95127560; PubMed=7826947;
 RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
 RT "Human Fas ligand: gene structure, chromosomal location and species
 RT specificity";
 RL Int. Immunol. 6:1567-1574 (1994).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Schaeublein C.E., Poehlmann R., Philippsen P., Ebel H.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).

RA MEDLINE=95071350; PubMed=7980502;
RA Mita E., Hayashi N., Ito S., Takehara T., Hijioka T., Kasahara A.,
RA Fusamoto H., Kamada T.,
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus
RT infection.";
RL Biochem. Biophys. Res. Commun. 204:468-474(1994).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocyte;
RA Zeytun A., Nagarkatti M., Nagarkatti P.S.;
RT "Isolation and characterization of a new naturally occurring variant of
RT human Fas ligand that is expressed only in membrane bound form.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Walkinson J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RA MEDLINE=22388257; PubMed=12477932;
RA Strassburg R.L., Feingold E.A., Grosse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Betrow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lonnellano N.A., Peters G.U., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.U., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villallon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey U., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Sherchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Blood;
RA Matsumura M., Nakanishi Y., Ohba Y.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [9]
RP CHARACTERIZATION, AND MUTAGENESIS OF PRO-206, TYR-218 AND PHE-275.
RX MEDLINE=97373583; PubMed=9228058;
RA Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scodetti P.,
RA Terkikh A., Peitsch M.C., Tschopp J.;
RT "Characterization of Fas (apo-1, CD95)-Fas ligand interaction.";
RL J. Biol. Chem. 272:18827-18833(1997).
RN [10]
RP PROCESSING.
RX MEDLINE=98087475; PubMed=9427603;
RA Tanaka M., Irai T., Adachi M., Nagata S.;
RT "Downregulation of Fas ligand by shedding.";
RL Nat. Med. 4:31-36(1998).
RP -1- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6/DCR3
CC modulates its effects.
CC -1- SUBUNIT: Homotrimer (Probable).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. May be released
CC into the extracellular fluid, probably by cleavage from the cell
CC surface.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;

CC		-Isoid=P48023-1; Sequence=Displayed;
CC	Name=2;	
CC	-Isoid=P48023-2; Sequence=VSP_006443, VSP_006444;	
CC	-PTM: N-glycosylated.	
CC	-PTM: The soluble form derives from the membrane form by proteolytic processing.	
CC	-DISEASE: Defects in TNFSF6 are a cause of autoimmune lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as Canale-Smith syndrome (CSS). ALPS is a childhood syndrome involving hemolytic anemia and thrombocytopenia with massive lymphadenopathy and splenomegaly.	
CC	-SIMILARITY: Belongs to the tumor necrosis factor family.	
CC	-! DATABASE: NAME=PROW; NOTE=PROW 2:59-69(2001); WWW="http://www.ncbi.nlm.nih.gov/prow/guide/333879674.g.htm".	
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CC	-----	
DR	EMBL; X89102; CAA61474.1; -	
DR	EMBL; U08137; AAC50071.1; -	
DR	EMBL; U11821; AAC50124.1; -	
DR	EMBL; D38182; BAA07320.1; -	
DR	EMBL; AF288573; AAG60017.1; -	
DR	EMBL; Z96050; CAB09424.1; -	
DR	EMBL; BC017502; AAH17502.1; -	
DR	EMBL; AB013303; BAA32542.1; -	
DR	PIR; I38707; I38707.	
DR	HSSP; P01375; ITNF.	
DR	Genew; HGNC:11936; TNFSF6.	
DR	MIM; 134638; -	
DR	GO; GO:0005887; C:integral to plasma membrane; TAS.	
DR	GO; GO:0005102; F:receptor binding; TAS.	
DR	GO; GO:0007267; P:cell-cell signalling; TAS.	
DR	GO; GO:0006917; P:induction of apoptosis; TAS.	
DR	GO; GO:0007165; P:signal transduction; TAS.	
DR	InterPro; IPRO06053; TNF_family.	
DR	InterPro; IPRO06052; TNF_family.	
DR	InterPro; IPRO08983; TNF_like.	
DR	InterPro; IPRO03636; TNF_subf.	
DR	Pfam; PF00229; TNF; 1.	
DR	PRINTS; PR01681; FASTIGAND.	
DR	PRINTS; PR01234; TNECROSISFCT.	
DR	Prodom; PD002012; TNF_subf; 1.	
DR	SMART; SM00207; TNF; 1.	
DR	PROSITE; PS00251; TNF_1; 1.	
KW	PROSITE; PS50049; TNF_2; 1.	
DV	Cycokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor; Alternative splicing; Antigen.	
FT	CHAIN	1 .. 281
FT		
FT	CHAIN	130 .. 281
FT		
FT	DOMAIN	1 .. 80
FT	TRANSMEM	81 .. 102
FT		
FT	DOMAIN	103 .. 281
FT	DOMAIN	4 .. 70
FT	SITE	129 .. 130
FT	DISULFID	202 .. 233
FT	CARBOHYD	184 .. 184
FT	CARBOHYD	250 .. 250
FT	CARBOHYD	260 .. 260
FT	VARSPLIC	117 .. 127
FT		
FT	/FTid=VSP_006443.	

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FT VARSPIC 128 281 Missing (in isoform 2).
FT MUTAGEN 206 206 /FTid=VSP_006444.
FT MUTAGEN 218 218 P->D,F,R: LOWERS BINDING TO TNFRSF6 AND
FT MUTAGEN 218 218 REDUCES CYTOTOXICITY MORE THAN 100-FOLD.
FT MUTAGEN 218 218 Y->F,R: LOWERS BINDING TO TNFRSF6 AND
FT MUTAGEN 218 218 ABOLISHES CYTOTOXICITY.
FT MUTAGEN 218 218 F->L: ABOLISHES BINDING TO TNFRSF6 AND
FT MUTAGEN 218 218 CYTOTOXICITY.
SQ SEQUENCE 281 AA; 31485 MW; ABA6B338246E9B CRC64;

Query Match 12.6%; Score 186; DB 1; Length 281;
Best Local Similarity 22.1%; Pred. No. 3.6e-08;
Matches 63; Conservative 54; Mismatches 82; Indels 86; Gaps 11;

QY 4 MEVGGPSLGGTCLVIVITVLQSLCVAV---TVYVTFNKLKQMDKXSKSGIACFLKE 60
DB 71 LKRGHNSGTG-LCLVMEFVVALVGLGFMFLHQLKELAEIRSTQWHTASSLEK 129
QY 61 DDSYMDPDESMNSPCWQVKNQRLQVLRKMLRTSEETSTVGEKQONISPLVRERGPQ 120
DB 130 QIGHSPPE-----KKELRKV----- 146
QY 121 RVAAHITGRGSRNTLSPNSKNEKALGRKINSWSSSGHSFLSNHLRNGELVHEKG 180
DB 147 ---AHLT---GKSNSRMP-----LEWEDT-YGIVLISGVYKKKGGLVINEGTG 187
QY 181 FYIYISQTFRPEELKENTKDKQWQYIY-KITSYDPDILMKASRNS-----CMSX 233
DB 188 LYFVYSKYVFRGQ-----SCNNLPLSHKVVYRNSKYPQDLVWMEGKMSYCTTGQMMAR 241
QY 234 DAEVGLYSIYGIGFELKENDRIFFVSVTNEHLIDMDHEASFFGAF 278
DB 242 -----SSTLGAVALNLSADHLVYVNSLSLVNPEBSGTFFGV 279

RESULT 9
TNF6_MACMU STANDARD; PRT; 280 AA.
ID TNF6_MACMU
AC Q9WT6; O9BDM5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
GN (CD95L protein).
OS TNFRSF6 OR FASL OR CD95L.
OS Macaca mulatta (Rhesus macaque), macaque (Cynomolgus monkey), and
OS Macaca fascicularis (Crab eating macaque).
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OC CBI_TaxID=9544, 9541, 9545;
[1]
SEQUENCE FROM N.A.
RP SPECIES=M.mulatta; TISSUE=Lymphocytes;
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RA "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
RN [2]
SEQUENCE FROM N.A.
RP SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
RA Kiril Y., Inoue T., Yoshino K.;
RA Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6/DCR3
CC modulates its effects (By similarity).

```

```

CC -!- SUBUNIT: Homotrimer (Potential).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC
DR EMBL; AF344856; AAA37539.1; -
DR EMBL; AB035138; BAA90294.1; -
DR EMBL; AB035139; BAA90295.1; -
DR EMBL; AB035140; BAA90296.1; -
DR HSSP; P01375; 4TSV.
DR InterPro; IPR008064; Fas_ligand.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
CHAIN 1 280
FT FT CHAIN 129 280
FT FT TRANSMEM 81 101
FT FT DOMAIN 102 280
FT FT DOMAIN 4 69
FT FT DOMAIN 128 129
FT FT SITE 128 129
FT FT DISULFID 201 232
FT FT CARBOHYD 183 183
FT FT CARBOHYD 249 249
FT FT CARBOHYD 259 259
FT FT CONFLICT 60 60
SQ SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;

Query Match 12.5%; Score 185; DB 1; Length 280;
Best Local Similarity 22.1%; Pred. No. 4.4e-08;
Matches 61; Conservative 56; Mismatches 91; Indels 68; Gaps 10;

QY 4 MEVGGPSLGGTCLVIVITVLQSLCVAVTVYVTFNKLKQMDKXSKSGIACFLKEDDS 63
DB 70 LKRGHNSGTG-LCLVMEFVVALVGLGFMFLHQLKELAE-----LRSST 118
QY 64 YMDPDESMNSPCWQVKNQRLQVLRKMLRTSEETSTVGEKQONISPLVRERGPQVA 123
DB 119 -----QKHTASLRLKQIGHSP-PPKKEGRKV 145
QY 124 AHTTGRGSRNTLSPNSKNEKALGRKINSWSSSGHSFLSNHLRNGELVHEKFFY 183
DB 146 AHLTG-----KPSRSRMP-----EWEDT-YGIVLISGVYKKKGGLVINEGTLYP 189
QY 184 IYQTFRFRPEELKENTKDKQWQYIY-KITSYDPDILMKASRNSCWGKDAEYGLYSI 242
DB 190 VYSKYVFRGQ-----SCNNLPLSHKVVYRNSKYPQDLVWMEGKMS-YCTTGQMMHSS 242
QY 243 YQGIPELKNDRIFVSVTNEHLIDMDHEASFFGAF 278

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Db 243 YIGAVENLTISADHLYVNVSELSLVNFESQTFEGLY 278

RESULT 10

TNFS CHICK STANDARD; PRT: 272 AA.

AC Q918D8; 28-FEB-2003 (Rel. 41, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-L) (CD154 protein).

GN TNFSF5 OR CD40LG OR CD40L.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OX NCBI_TaxID=9031;

RN [1]

RC SEQUENCE FROM N.A.

RA STRAIN=White leghorn; TISSUE=Spleen;

RT Tregaskes C.A., Young J.R., Burnside J.;

RT "Cloning of a putative chicken CD40 ligand."

RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IgR production in the presence of IL-4. Involved in immunoglobulin class switching (by similarity).

CC -1- SUBUNIT: Homotrimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).

CC -1- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.

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CC

DR EMBL; AJ243435; CAB95748.2; --

DR HSSP; P29965; IAIY.

DR GO; GO:0016021; C:integral to membrane; ISS.

DR GO; GO:0005174; P:CD40 receptor binding; ISS.

DR GO; GO:0042100; P:B-cell proliferation; ISS.

DR GO; GO:0006954; P:inflammatory response; ISS.

DR GO; GO:0007159; P:leukocyte cell adhesion; ISS.

DR GO; GO:0030168; P:platelet activation; ISS.

DR InterPro; IPR003263; TNF_5.

DR InterPro; IPR006052; TNF_family.

DR InterPro; IPR008983; TNF_like.

DR InterPro; IPR003636; TNF_subf.

DR Pfam; PF00229; TNF_1.

DR PRINTS; PR01702; CD40LG.DND.

DR ProDom; PD008600; TNF_5.1.

DR ProDom; PD002012; TNF_subf; 1.

DR SMART; SM00207; TNF_1.

DR PROSITE; PS00251; TNF_1; 1.

DR PROSITE; PS00049; TNF_2; 1.

DR CysKline; Transmembrane; Glycoprotein; Signal-anchor.

FT CHAIN 1 272 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 5, MEMBRANE FORM.

FT CHAIN 111 272 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 5, SOLUBLE FORM (BY SIMILARITY).

FT TRANSMEM 24 44 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).

FT DOMAIN 45 272 EXTRACELLULAR (POTENTIAL).

FT SITE 110 111 CLEAVAGE (BY SIMILARITY).

FT DISULFID 190 229 POTENTIAL.

FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 272 AA; 30832 MW; 8CD0338A924E044B CRC64;

Query Match 12.4%; Score 184; DB 1; Length 272;

Best local similarity 25.4%; Pred. No. 5.1e-08;

Matches 69; Conservative 48; Mismatches 119; Indels 36; Gaps 9;

QY 16 CVLIVITVTLQSLCVAVTVYFTNELKQMDKXSKSGIACFLKEDDSYWPNDSESNWS 75

DB 26 CFLSVFVWV--QITGTVLFCILYHMKMDKKEBVLSTNEDYIFLAKYQCKQGEQKSTLL 83

QY 76 PCWQVKKQLQVIRKMLRTSEELTISVQEKQNTISPLVBERGP-----QFVAHIT 127

DB 84 DCEKVLKGFDDLOCKD--RTASEELPFEMHRRGHEHFLKSRNBTSAVEERQPIATHLA 141

QY 128 GTRGRSNTLSSPNSKNEKALGRKINSW-ESSRSQHSPLSLHLRNGELVTHEKGFYITYS 186

DB 142 GV--KSNITV-----RVLKMTTISYAPTSLISYH--EGDLKVEKKGLEYIYS 185

QY 187 QTFPRQOEIKENTKDKQNVQYIYXTSYDPDILLKKSARNSQWSKDAEYGLYSYOG 246

DB 186 QVSF-----CTRAASAPFTLYIYLYLPWEEDRLMKGLDHTST--TALCELQSTREGG 238

QY 247 IFELEKNDRIFFSVTNEHLIDMDHEASFGAF 278

DB 239 VFELRGDMVFVAVDTSTAVVAVPGVTFRGMP 270

RESULT 11

TNFS PIG STANDARD; PRT: 282 AA.

AC Q9BEA8; Q95W04; Q95N10;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 6 (Fas antigen ligand).

GN TNFSF6 OR FASL.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINB-21322533; PubMed=11429161;

RA Muneta Y., Shimoji Y., Imamura S., Mori Y.;

RT "Molecular cloning, characterization, and expression of porcine Fas ligand (CD95 ligand)."

RT J. Interferon Cytokine Res. 21:305-312 (2001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Guanxi bama miniature pig;

RA Zhu N., Young Y.;

RT "Molecular cloning and characterization of porcine Fas ligand cDNA."

RT Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC Tissue=Lymphoid;

RA Tsubaki S., Kono M., Bloom E.T.;

RT "Cloning and potential utility of porcine Fas ligand: overexpression in porcine cells protects them from attack by human cytolytic cells."

RT Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=Landrace x Large Yorkshire white; TISSUE=Thymocytes;

RX MEDLINE=21653191; PubMed=11792426;

RA Moregi-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;

RT "Porcine Fas-Ligand gene: genomic sequence analysis and comparison with human gene."

RT Mol. Immunol. 38:561-566 (2002).

CC -1- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that


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FT FT DOMAIN 1 77 MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT FT TRANSMEM 78 99 CYTOPLASMIC (POTENTIAL).
FT FT DOMAIN 100 278 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT SITE 4 69 (POTENTIAL).
FT FT SITE 126 127 EXTRACELLULAR (POTENTIAL).
FT FT DISULFID 126 127 PRO-RICH.
FT FT CARBOHYD 116 116 POLY-PRO.
FT FT CARBOHYD 116 116 CLEAVAGE (BY SIMILARITY).
FT FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 278 AA; 31140 MW; 2898E18A62CEAC6 CRC64;

Query Match 12.0%; Score 177.5; DB 1; Length 278;
Best Local Similarity 27.5%; Pred. No. 1.8e-07;
Matches 50; Conservative 39; Mismatches 64; Indels 29; Gaps 8;

QY 100 ISTVOEQKQNTSPYRBERGPORVAHITGT-RGRSNTLSSPNSKNEALGRKINSWSSR 158
DQ 121 VSSFEQKQNPSTSETKKRSV-AHITGNPRSHITP-----EMEDT- 162
QY 159 SGHSFSLNHLRNGELVHEKGFYIYSQTYFRFOEBIKENTKDKOMVQIY-KYTSYP 217
DQ 163 YGTALISGVKKKGLVINEAGLYFYVSKYFRGQ-----SCNSQPLSHKVMKPKY 216
QY 218 DPLIMKSAR-NSGWSKDAEYGLVSIYOGGIFELKENDRIFVSYTNHLLDMDEHSAFPG 276
DQ 217 GDVLVMEKKKINCTT--GGIMHSSYLAENVLTADHLVYVINSQSLINFEESKTFPG 274
QY 277 AF 278
DQ 275 LY 276

RESULT 13
TNF5_BOVIN STANDARD; PRT; 261 AA.
ID TNF5_BOVIN STANDARD; PRT; 261 AA.
AC P51749;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (TNF-
DE related activation protein) (TRAP) (T cell antigen GP39).
GN TNF5 OR CD40LG OR CD40L.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=9600582; PubMed=7590981;
RA Merrens B.B.L.C.; Murtuki M.; Gaidulis L.;
RT "Cloning of two members of the TNF superfamily in cattle: CD40 ligand
RT and tumor necrosis factor alpha."
RL Immunogenetics 42:430-431(1995).
CC -I- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC proliferation in the absence of co-stimulus as well as IgE
CC production in the presence of IL-4. Involved in immunoglobulin
CC class switching (By similarity).
CC -I- SUBUNIT: Homotrimer (By similarity).
CC -I- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -I- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -I- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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CC -----
DR EMBL; Z48469; CAAB8363.1; -.
DR PIR; S53090; S53090.
DR HSSP; E29965; 1ALV.
DR GO; GO:0016021; C:integral to membrane; ISS.
DR GO; GO:0005174; F:CD40 receptor binding; ISS.
DR GO; GO:0042100; P:B-cell proliferation; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0007159; P:leukocyte cell adhesion; ISS.
DR GO; GO:0030168; P:platelet activation; ISS.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01702; CD40LIGAND.
DR ProDom; PD008600; TNF_5; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF_1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT FT CHAIN 1 261
FT FT CHAIN 113 261
FT FT DOMAIN 1 22
FT FT TRANSMEM 23 46
FT FT SITE 112 113
FT FT DISULFID 178 218
FT FT CARBOHYD 240 240
SQ SEQUENCE 261 AA; 29242 MW; 8491FEFB30A787FD CRC64;

Query Match 11.1%; Score 164; DB 1; Length 261;
Best Local Similarity 25.9%; Pred. No. 2.2e-06;
Matches 72; Conservative 52; Mismatches 114; Indels 40; Gaps 14;

QY 6 VOGGSLGQTCVILVFTLL--QSLCAVTVYFTNEKQMDKXSGIAQLEDDSD 63
DQ 13 VATGPPVSMK-IPWLLVLTFTOMIGSLPFAVYLRDKIEDENLHDFVFK--T 68
QY 64 YNDPNDSESMG--PCWQVKQOLROIVRMILRTSEETISTYOEKQNTSPYRBERGPOR 121
DQ 69 IQRCKRGESLSLNCERIRSFEDLV-KDIQNK-----VKKKKNFEMKGDQEPQ 121
QY 122 VAHITGTRGSENTLSSPNSKNEALGRKINSWSSRSGHSTLSN--LHNRG-ELVTHE 178
DQ 122 IAAHV-----ISEASKTTSVL-----QW--APKGYITLSNLTVLENGKQLAVAR 165
QY 179 KGFYIYSQTYFRFOEBIKENTKDKOMVQIYKYTSYDPLIMKSARNSCWSKDAEY 238
DQ 166 QGFYIYIQVFCNSR-----TLGAPFLASCLKSPSGSEHILIRANHTSSSKPC--G 219
QY 239 LYSIYOGGIFELKENDRIFVSYTNHLLDMDEHSAFPG 276
DQ 220 QQSIIHGVFELQSGASVFVNTDPSQVSHGTGFTSPFG 257

RESULT 14
TN15_HUMAN STANDARD; PRT; 174 AA.
ID TN15_HUMAN
AC O95150;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 15 (Vascular
DE endothelial cell growth inhibitor) (TNF ligand-related molecule 1).
GN TNF5 OR VEGI OR TLI.

```

OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=umbilical vein;
 RA MEDLINE=98091541; PubMed=9872942;
 RX Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C.,
 RA Janat F., Kozak D., Xu S., Rojas L., Aggarwal B.B., Ruben S.,
 RA Li L.-Y., Gentz R., Yu G.-L.,
 RA "VEG1, a novel cytokine of the tumor necrosis factor family, is an
 angiogenesis inhibitor that suppresses the growth of colon carcinomas
 in vivo.";
 RL FASEB J. 13:181-189(1999).
 CC -1- FUNCTION: Inhibits vascular endothelial growth and angiogenesis
 (in vitro).
 CC -1- SUBUNIT: Homotrimer (Potential).
 CC -1- TISSUE SPECIFICITY: Type II membrane protein (Probable).
 CC -1- TISSUE SPECIFICITY: Specifically expressed in endothelial cells.
 CC Detected in placenta, lung, kidney, skeletal muscle, pancreas,
 CC spleen, prostate, small intestine and colon.
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AF039390; AAD08783.1; -
 DR HSSP: P50591; ID06; TNFSF15.
 DR Genew: HGNC:11931; TNFSF15.
 DR MIM: 604052; -
 DR GO: GO:0005887; C:integral to plasma membrane; TAS.
 DR GO: GO:0005102; F:receptor binding; TAS.
 DR GO: GO:0000704; P:regulation of cell cycle; TAS.
 DR InterPro: IPR006053; TNF_abc.
 DR InterPro: IPR006052; TNF_family.
 DR InterPro: IPR008983; TNF_like.
 DR InterPro: IPR003636; TNF_subf.
 DR Pfam: PF00229; TNF_1.
 DR PRINTS: PR01234; TNECROSISFCR.
 DR PRODOM: PD002012; TNF_subf; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
 FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 13 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 26 174 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 85 125 POTENTIAL.
 FT CARBOHYD 56 56 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 152 152 N-LINKED (GLCNAC...) (POTENTIAL).
 SO SEQUENCE 174 AA; 20131 MW; CCB83BA7EB673B98 CRC64;
 Query Match 10.8%; Score 160; DB 1; Length 174;
 Best local similarity 35.3%; Pred. No. 2,7e-06;
 Matches 49; Conservative 24; Mismatches 48; Indels 18; Gaps 8;

RESULT 15
 ID TN14_HUMAN STANDARD; PRT; 240 AA.
 AC O43557; 075476; Q8WV8; Q96LD2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 14 (Herpesvirus entry
 mediator-ligand) (HVEML).
 GN TNFSF14 OR LIGHT OR HVEML.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RX MEDLINE=98122340; PubMed=9462508;
 RA Mauri D.N., Eber R., Montgomery R.I., Kochel K.D., Cheung T.C.,
 RA Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,
 RA Ware C.F.;
 RT "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are
 RT ligands for herpesvirus entry mediator.";
 RL Immunity 8:21-30(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RC TISSUE=Liver;
 RX MEDLINE=98438532; PubMed=9765287;
 RA Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J.,
 RA Tan K.B., Dede K., Spampinato J., Silberman C., Hensley P.,
 RA DiPinzio R., Emery J.G., Deen K., Eichen C., Chabot-Fletcher M.,
 RA Truneh A., Young P.R.;
 RT "Herpesvirus entry mediator ligand (HVEML), a novel ligand for
 RT HVEML/TR2, stimulates proliferation of T cells and inhibits HT29 cell
 RT growth.";
 RL J. Biol. Chem. 273:27548-27556(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND PROCESSING.
 RX MEDLINE=21528948; PubMed=11673523;
 RA Granger S.W., Butrovich K.D., Houshmand P., Edwards W.R., Ware C.F.;
 RT "Genomic characterization of LIGHT reveals linkage to an immune
 RT response locus on chromosome 19p13.3 and distinct isoforms generated
 RT by alternate splicing or proteolysis.";
 RL J. Immunol. 167:5122-5128(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Mausius K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cassavani T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarnatone P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Huiy S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitley M., Madan A., Young A.C., Green E.D., Dickson M.C.,
 RA Blakeley R.W., Touchman J.W., Myers R.M.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF3/LTBR. Binding to the
 CC decoy receptor TNFRSF6B modulates its effects. Activates NFkB,
 CC stimulates the proliferation of T cells, and inhibits growth of
 CC the adenocarcinoma HT-29. Acts as a receptor for Herpes simplex

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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:23:31; Search time 17 Seconds

(without alignments)
853.347 Million cell updates/sec

Title: US-10-662-431-2

Perfect score: 1478
Sequence: 1 MAMEVQGGPSLGTCVIV.....NEHLIDMHASFFGAFIVG 281

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1478	100.0	281	1	US-08-670-354-2
2	1478	100.0	281	3	US-08-584-031-1
3	1478	100.0	281	3	US-08-780-496-1
4	1478	100.0	281	3	US-08-883-086-10
5	1478	100.0	281	3	US-09-320-424-2
6	1478	100.0	281	4	US-09-333-593A-6
7	1478	100.0	281	4	US-09-157-864-11
8	1478	100.0	281	4	US-09-825-563-2
9	1478	100.0	281	4	US-10-039-785-66
10	1478	100.0	281	5	PCT-US96-10895-2
11	1469	99.4	279	4	US-09-072-993C-3
12	988	66.8	253	4	US-09-320-424-11
13	988	66.8	253	4	US-09-825-563-11
14	988	66.8	256	3	US-09-320-424-13
15	988	66.8	256	4	US-09-825-563-13
16	930	62.9	177	3	US-09-105-343A-7
17	930	62.9	291	1	US-08-670-354-6
18	930	62.9	291	3	US-09-320-424-6
19	930	62.9	291	4	US-09-825-563-6
20	930	62.9	291	5	PCT-US96-10895-6
21	850	57.5	161	4	US-09-565-423-7
22	654	44.2	183	3	US-09-105-343A-8
23	482	32.6	101	1	US-08-670-354-4
24	482	32.6	101	3	US-09-320-424-4
25	482	32.6	101	4	US-09-825-563-4
26	482	32.6	101	5	PCT-US96-10895-4
27	446	30.2	85	4	US-09-632-287A-12

28	258.5	17.5	294	3	US-08-996-139-11	Sequence 11, Appl
29	258.5	17.5	294	3	US-08-995-659-11	Sequence 11, Appl
30	258.5	17.5	294	3	US-09-215-649A-11	Sequence 11, Appl
31	258.5	17.5	294	4	US-09-577-780-11	Sequence 11, Appl
32	258.5	17.5	294	4	US-09-577-800-11	Sequence 11, Appl
33	258.5	17.5	294	4	US-09-466-496-11	Sequence 11, Appl
34	258.5	17.5	294	4	US-09-871-856-11	Sequence 11, Appl
35	258.5	17.5	294	4	US-09-871-291-11	Sequence 11, Appl
36	258.5	17.5	294	4	US-09-877-650-11	Sequence 11, Appl
37	258.5	17.5	316	2	US-08-842-842-7	Sequence 7, Appl
38	258.5	17.5	316	3	US-08-989-362-2	Sequence 2, Appl
39	258.5	17.5	316	4	US-09-052-521C-2	Sequence 2, Appl
40	258.5	17.5	316	4	US-09-671-658A-2	Sequence 2, Appl
41	258.5	17.5	316	4	US-09-396-937-4	Sequence 4, Appl
42	258.5	17.5	316	4	US-09-396-937-6	Sequence 6, Appl
43	251.5	17.0	317	3	US-08-996-139-13	Sequence 13, Appl
44	251.5	17.0	317	3	US-08-995-659-13	Sequence 13, Appl
45	251.5	17.0	317	3	US-09-215-649A-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-670-354-2
Sequence 2, Application US/08670354
Patent No. 5763223

GENERAL INFORMATION:

APPLICANT: Steven R. Wiley and

APPLICANT: Raymond G. Goodwin.

TITLE OF INVENTION: Cytokine That Induces Apoptosis

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESS: Kathryn A. Anderson, Immunex Corporation

SECRET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple 7.5.2

SOFTWARE: Microsoft Word, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/670,354

FILING DATE: 25-JUN-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/548,368

FILING DATE: 01-NOV-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Anderson, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2835-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 281 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-670-354-2

Query Match 100.0%, Score 1478, DB 1, Length 281,

Best Local Similarity 100.0%; Pred. No. 2,7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
QY 61 DDSTWDPNDESMNSPCWQVQWOLRQVLRKMLRTSEETITVQEKQONISPLVBERGPQ 120
DB 61 DDSTWDPNDESMNSPCWQVQWOLRQVLRKMLRTSEETITVQEKQONISPLVBERGPQ 120
QY 121 RVAAHITGRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILMKSAKNSCKDAEYGLY 240
DB 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILMKSAKNSCKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFFVSVTNEHLIDMDHEASFFGAFVWG 281
DB 241 SIYGGIFELKENDRIFFVSVTNEHLIDMDHEASFFGAFVWG 281

RESULT 2
US-08-584-031-1
Sequence 1, Application US/08584031A

Patent No. 6030945
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/08/584,031A
CURRENT FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
US-08-584-031-1

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2,7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
QY 61 DDSTWDPNDESMNSPCWQVQWOLRQVLRKMLRTSEETITVQEKQONISPLVBERGPQ 120
DB 61 DDSTWDPNDESMNSPCWQVQWOLRQVLRKMLRTSEETITVQEKQONISPLVBERGPQ 120
QY 121 RVAAHITGRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILMKSAKNSCKDAEYGLY 240
DB 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILMKSAKNSCKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFFVSVTNEHLIDMDHEASFFGAFVWG 281
DB 241 SIYGGIFELKENDRIFFVSVTNEHLIDMDHEASFFGAFVWG 281

RESULT 3
US-08-780-496-1
Sequence 1, Application US/08780496
Patent No. 6046048
GENERAL INFORMATION:
APPLICANT: Avi Ashkenazi, Aron Chuntharapai, Kyung Jin Kim

TITLE OF INVENTION: APO-2 Ligand
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California

COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/780,496

FILING DATE: 08-Jan-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P0978P1

TELEPHONE: 415/225-5416

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 281 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-780-496-1
Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2,7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
QY 61 DDSTWDPNDESMNSPCWQVQWOLRQVLRKMLRTSEETITVQEKQONISPLVBERGPQ 120
DB 61 DDSTWDPNDESMNSPCWQVQWOLRQVLRKMLRTSEETITVQEKQONISPLVBERGPQ 120
QY 121 RVAAHITGRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILMKSAKNSCKDAEYGLY 240
DB 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILMKSAKNSCKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFFVSVTNEHLIDMDHEASFFGAFVWG 281
DB 241 SIYGGIFELKENDRIFFVSVTNEHLIDMDHEASFFGAFVWG 281

RESULT 4
US-08-883-086-10
Sequence 10, Application US/08883086

Patent No. 6171787

GENERAL INFORMATION:

APPLICANT: WILEY, STEVEN

TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL

FOR TREATMENT AND DIAGNOSIS OF DISEASE

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,086
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6134, US, 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-0378
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6171787e
US-08-863-086-10

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2,7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVOGGSLSGQTCVLIVIFVLLQSLCAVAVYVYFTNELKQMDKYSKGIACFLKE 60
DB 1 MAMMEVOGGSLSGQTCVLIVIFVLLQSLCAVAVYVYFTNELKQMDKYSKGIACFLKE 60
QY 61 DSYWDPNDESNMNSPCQYKQRLQRLVRKMLITSEETSTVOEKQNTSPLYREGRQ 120
DB 61 DSYWDPNDESNMNSPCQYKQRLQRLVRKMLITSEETSTVOEKQNTSPLYREGRQ 120
QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLNGLVYHEKG 180
DB 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLNGLVYHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFIVG 281
DB 241 SIYGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFIVG 281

RESULT 5
US-09-320-424-2
Sequence 2, Application US/09320424
Patent No. 6284236
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: Cytochrome that Induces Apoptosis
FILE REFERENCE: 2835-B
CURRENT APPLICATION NUMBER: US/09/320,424
PRIOR FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER FILING DATE: 1998-11-10
EARLIER APPLICATION NUMBER: 09/048,641
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/670,354
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 08/548,368

100% 100%

EARLIER FILING DATE: 1995-11-01
EARLIER APPLICATION NUMBER: 08/496,632
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 281
TYPE: PRT
ORGANISM: human
US-09-320-424-2

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2,7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVOGGSLSGQTCVLIVIFVLLQSLCAVAVYVYFTNELKQMDKYSKGIACFLKE 60
DB 1 MAMMEVOGGSLSGQTCVLIVIFVLLQSLCAVAVYVYFTNELKQMDKYSKGIACFLKE 60
QY 61 DSYWDPNDESNMNSPCQYKQRLQRLVRKMLITSEETSTVOEKQNTSPLYREGRQ 120
DB 61 DSYWDPNDESNMNSPCQYKQRLQRLVRKMLITSEETSTVOEKQNTSPLYREGRQ 120
QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLNGLVYHEKG 180
DB 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLNGLVYHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFIVG 281
DB 241 SIYGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFIVG 281

RESULT 6
US-09-333-593A-6
Sequence 6, Application US/09333593A
Patent No. 6313269
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH C.
APPLICANT: YOUNG, PETER R.
APPLICANT: MARSHALL, LISA A.
APPLICANT: ROSHAK, AMY K.
APPLICANT: TAN, KONG B.
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
TITLE OF INVENTION: TR6
FILE REFERENCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333,593A
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 08/853,684
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 281
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-333-593A-6

100% 100%

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2,7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVOGGSLSGQTCVLIVIFVLLQSLCAVAVYVYFTNELKQMDKYSKGIACFLKE 60
DB 1 MAMMEVOGGSLSGQTCVLIVIFVLLQSLCAVAVYVYFTNELKQMDKYSKGIACFLKE 60

QY 61 DDSYWDPNDESNMSPCQVQWKQRLQVLRKMLRTSEETISTVOEKQONISPLVREBGPQ 120
DB 61 DDSYWDPNDESNMSPCQVQWKQRLQVLRKMLRTSEETISTVOEKQONISPLVREBGPQ 120
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVYHEKG 180
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVYHEKG 180
QY 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPPIILMKSAARNSCWSKDAEYGLY 240
DB 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPPIILMKSAARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 7
US-09-157-864-11
; Sequence 11, Application US/09157864
; Patent No. 6440694
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mille, Cynthia J
; APPLICANT: Jones, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,864
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 6111.N CN1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-157-864-11

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149; Indels 0; Gaps 0;
Matches 281; Conservative 0; Mismatches 0;

QY 1 MAMMEVQGGPSLIGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLIGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDESNMSPCQVQWKQRLQVLRKMLRTSEETISTVOEKQONISPLVREBGPQ 120
DB 61 DDSYWDPNDESNMSPCQVQWKQRLQVLRKMLRTSEETISTVOEKQONISPLVREBGPQ 120

under wild

Ad

QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVYHEKG 180
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVYHEKG 180
QY 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPPIILMKSAARNSCWSKDAEYGLY 240
DB 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPPIILMKSAARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 8
US-09-825-563-2
; Sequence 2, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Willey, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytochrome that Induces Apoptosis
; FILE REFERENCE: 2835-B
; CURRENT APPLICATION NUMBER: US/09/825,563
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
; US-09-825-563-2

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLIGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLIGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDESNMSPCQVQWKQRLQVLRKMLRTSEETISTVOEKQONISPLVREBGPQ 120
DB 61 DDSYWDPNDESNMSPCQVQWKQRLQVLRKMLRTSEETISTVOEKQONISPLVREBGPQ 120
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVYHEKG 180
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVYHEKG 180
QY 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPPIILMKSAARNSCWSKDAEYGLY 240
DB 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPPIILMKSAARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 9
US-10-039-785-66
; Sequence 66, Application US/10039785

Patent No. 6538938
 GENERAL INFORMATION:
 APPLICANT: Salcedo et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
 TITLE OF INVENTION: Receptors
 FILE REFERENCE: PFS50
 CURRENT APPLICATION NUMBER: US/10/039,785
 CURRENT FILING DATE: 2002-05-07
 PRIOR APPLICATION NUMBER: 60/369,860
 PRIOR FILING DATE: 2002-04-05
 PRIOR APPLICATION NUMBER: 60/341,237
 PRIOR FILING DATE: 2001-12-20
 PRIOR APPLICATION NUMBER: 60/331,310
 PRIOR FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/331,044
 PRIOR FILING DATE: 2001-11-07
 PRIOR APPLICATION NUMBER: 60/327,364
 PRIOR FILING DATE: 2001-10-09
 PRIOR APPLICATION NUMBER: 60/323,807
 PRIOR FILING DATE: 2001-09-21
 PRIOR APPLICATION NUMBER: 60/309,176
 PRIOR FILING DATE: 2001-08-02
 PRIOR APPLICATION NUMBER: 60/294,981
 PRIOR FILING DATE: 2001-06-04
 PRIOR APPLICATION NUMBER: 60/293,473
 PRIOR FILING DATE: 2001-05-25
 NUMBER OF SEQ ID NOS: 66
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 66
 LENGTH: 281
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-039-785-66

Query Match 100.0%; Score 1478; DB 4; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.7e-149;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAMMEVQGGPSLGGTCVLIVIFVLLQSLCAVATYVYFNEELKQMDKYSKSGIACFLKE 60
 1 MAMMEVQGGPSLGGTCVLIVIFVLLQSLCAVATYVYFNEELKQMDKYSKSGIACFLKE 60
 61 DSYNDPNDDESMSNCPQVQKQRLQVYKMLIRTSSEITISVQEKQNIISPLVERGQ 120
 61 DSYNDPNDDESMSNCPQVQKQRLQVYKMLIRTSSEITISVQEKQNIISPLVERGQ 120
 121 RVAAHITGRGSNTLSSPNSKNEKALGRKINSWSSSRSGHSFLSNLHRLNGELVIHEKG 180
 121 RVAAHITGRGSNTLSSPNSKNEKALGRKINSWSSSRSGHSFLSNLHRLNGELVIHEKG 180
 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYPPDILMKSAKNSCWSKDAEYGLY 240
 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYPPDILMKSAKNSCWSKDAEYGLY 240
 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 10 PCT-US96-10895-2

Sequence 2, Application PC/TUS9610895
 GENERAL INFORMATION:
 APPLICANT: Immunex Corporation.
 TITLE OF INVENTION: Cyclokin That Induces Apoptosis
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple 7.5.2
 SOFTWARE: Microsoft Word, Version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/10895
 FILING DATE: 25-JUN-1996
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/496,632
 FILING DATE: 29-JUN-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/548,368
 FILING DATE: 01-NOV-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Anderson, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2835-WO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 281 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US96-10895-2

Query Match 100.0%; Score 1478; DB 5; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.7e-149;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAMMEVQGGPSLGGTCVLIVIFVLLQSLCAVATYVYFNEELKQMDKYSKSGIACFLKE 60
 1 MAMMEVQGGPSLGGTCVLIVIFVLLQSLCAVATYVYFNEELKQMDKYSKSGIACFLKE 60
 61 DSYNDPNDDESMSNCPQVQKQRLQVYKMLIRTSSEITISVQEKQNIISPLVERGQ 120
 61 DSYNDPNDDESMSNCPQVQKQRLQVYKMLIRTSSEITISVQEKQNIISPLVERGQ 120
 121 RVAAHITGRGSNTLSSPNSKNEKALGRKINSWSSSRSGHSFLSNLHRLNGELVIHEKG 180
 121 RVAAHITGRGSNTLSSPNSKNEKALGRKINSWSSSRSGHSFLSNLHRLNGELVIHEKG 180
 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYPPDILMKSAKNSCWSKDAEYGLY 240
 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYPPDILMKSAKNSCWSKDAEYGLY 240
 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 11

US-09-072-993C-3
 Sequence 3, Application US/09072993C
 Patent No. 6346388
 GENERAL INFORMATION:
 APPLICANT: Michael R. Young
 TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
 TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
 FILE REFERENCE: GH-50030
 CURRENT APPLICATION NUMBER: US/09/072,993C
 CURRENT FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/055,513
 PRIOR FILING DATE: 1997-08-13
 PRIOR APPLICATION NUMBER: 60/056,980

PRIOR FILING DATE: 1997-08-26
 PRIOR APPLICATION NUMBER: 60/057,550
 PRIOR FILING DATE: 1997-08-29
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 3
 LENGTH: 279
 TYPE: PRT
 ORGANISM: HOMO SAPIENS
 US-09-072-993C-3

Query Match 99.4%; Score 1469; DB 4; Length 279;
 Best Local Similarity 100.0%; Pred. No. 2.5e-148;
 Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MMEVGGGSLGQTCVLIIVFTVLLQSLCAVAVYVYFNNELKQMDKYSKGIACFLKEDD 62
 DB 1 MMEVGGGSLGQTCVLIIVFTVLLQSLCAVAVYVYFNNELKQMDKYSKGIACFLKEDD 60
 QY 63 SYMDPNDESMNSPCWQVKMQLRQIVRKMLITSEETISTVOEKQONISPLVREKGPORV 122
 DB 61 SYMDPNDESMNSPCWQVKMQLRQIVRKMLITSEETISTVOEKQONISPLVREKGPORV 120
 QY 123 AAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHLRNGELVHEKGFY 182
 DB 121 AAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHLRNGELVHEKGFY 180
 QY 183 YTSQTYRFRQEIENKTKNDKQWQYIYKYTSYDPDILMKSARNSCWSKDAEYGLYSI 242
 DB 181 YTSQTYRFRQEIENKTKNDKQWQYIYKYTSYDPDILMKSARNSCWSKDAEYGLYSI 240
 QY 243 YQGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 DB 241 YQGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 279

RESULT 12
 US-09-320-424-11
 Sequence 11, Application US/09320424
 Patent No. 6284236
 GENERAL INFORMATION:
 APPLICANT: Wiley, Steven R.
 APPLICANT: Goodwin, Raymond G.
 TITLE OF INVENTION: Cytochrome that Induces Apoptosis
 FILE REFERENCE: 2835-E
 CURRENT APPLICATION NUMBER: US/09/320,424
 EARLIER FILING DATE: 1999-05-26
 EARLIER APPLICATION NUMBER: 09/190,046
 EARLIER FILING DATE: 1998-11-10
 EARLIER APPLICATION NUMBER: 09/048,641
 EARLIER FILING DATE: 1998-03-26
 EARLIER APPLICATION NUMBER: 08/670,354
 EARLIER FILING DATE: 1996-06-25
 EARLIER APPLICATION NUMBER: 08/548,368
 EARLIER FILING DATE: 1995-11-01
 EARLIER APPLICATION NUMBER: 08/496,632
 EARLIER FILING DATE: 1995-06-29
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 11
 LENGTH: 253
 TYPE: PRT
 ORGANISM: synthetic fusion
 US-09-320-424-11

Query Match 66.8%; Score 988; DB 3; Length 253;
 Best Local Similarity 78.9%; Pred. No. 4.3e-97;
 Matches 194; Conservative 15; Mismatches 13; Indels 24; Gaps 2;
 QY 39 TNEIKQMDKYSKGIACFLKEDDSYMDPNDESMNSPCWQVK--WQLRQIVRKMLIRT 95
 DB 29 SDRMKQIEDKI-----EELISKYIHENEIARIKKLIGERTST 67

QY 96 SEETISTVOEKQONISPLVREKGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWE 155
 DB 68 SEETISTVOEKQONISPLVREKGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWE 127
 QY 156 SSRGSHFLSNLHLRNGELVHEKGFYIYSQTYRFRQEIENKTKNDKQWQYIYKTS 215
 DB 128 SSRGSHFLSNLHLRNGELVHEKGFYIYSQTYRFRQEIENKTKNDKQWQYIYKTS 187
 QY 216 YPDPIILMKSARNSCWSKDAEYGLYSIYQGI FELKENDRIFVSVTNEHLIDMDHEASFF 275
 DB 188 YPDPIILMKSARNSCWSKDAEYGLYSIYQGI FELKENDRIFVSVTNEHLIDMDHEASFF 247
 QY 276 GAFLVG 281
 DB 248 GAFLVG 253

RESULT 13
 US-09-825-563-11
 Sequence 11, Application US/09825563
 Patent No. 6521228
 GENERAL INFORMATION:
 APPLICANT: Wiley, Steven R.
 APPLICANT: Goodwin, Raymond G.
 TITLE OF INVENTION: Cytochrome that Induces Apoptosis
 FILE REFERENCE: 2835-E
 CURRENT APPLICATION NUMBER: US/09/825,563
 PRIOR FILING DATE: 2001-04-02
 PRIOR APPLICATION NUMBER: 09/320,424
 PRIOR FILING DATE: 1999-05-26
 PRIOR APPLICATION NUMBER: 09/190,046
 PRIOR FILING DATE: 1998-11-10
 PRIOR APPLICATION NUMBER: 09/048,641
 PRIOR FILING DATE: 1998-03-26
 PRIOR APPLICATION NUMBER: 08/670,354
 PRIOR FILING DATE: 1996-06-25
 PRIOR APPLICATION NUMBER: 08/548,368
 PRIOR FILING DATE: 1995-11-01
 PRIOR APPLICATION NUMBER: 08/496,632
 PRIOR FILING DATE: 1995-06-29
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 11
 LENGTH: 253
 TYPE: PRT
 ORGANISM: synthetic fusion
 US-09-825-563-11

Query Match 66.8%; Score 988; DB 4; Length 253;
 Best Local Similarity 78.9%; Pred. No. 4.3e-97;
 Matches 194; Conservative 15; Mismatches 13; Indels 24; Gaps 2;
 QY 39 TNEIKQMDKYSKGIACFLKEDDSYMDPNDESMNSPCWQVK--WQLRQIVRKMLIRT 95
 DB 29 SDRMKQIEDKI-----EELISKYIHENEIARIKKLIGERTST 67
 QY 96 SEETISTVOEKQONISPLVREKGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWE 155
 DB 68 SEETISTVOEKQONISPLVREKGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWE 127
 QY 156 SSRGSHFLSNLHLRNGELVHEKGFYIYSQTYRFRQEIENKTKNDKQWQYIYKTS 215
 DB 128 SSRGSHFLSNLHLRNGELVHEKGFYIYSQTYRFRQEIENKTKNDKQWQYIYKTS 187
 QY 216 YPDPIILMKSARNSCWSKDAEYGLYSIYQGI FELKENDRIFVSVTNEHLIDMDHEASFF 275
 DB 188 YPDPIILMKSARNSCWSKDAEYGLYSIYQGI FELKENDRIFVSVTNEHLIDMDHEASFF 247
 QY 276 GAFLVG 281
 DB 248 GAFLVG 253

Query Match	66.8%	Score 988	DB 3	Length 256,
Best Local Similarity	78.9%	Pred. No. 4.4e-97,		
Matches 194; Conservative	15;	Mismatches 13;	Indels 24;	Gaps 2

RESULT 15
 US-09-825-563-13
 : Sequence 13, Application US/09825563
 : Patent No. 6521228
 : GENERAL INFORMATION:
 : APPLICANT: Wiley, Steven R.
 : APPLICANT: Goodwin, Raymond G.
 : TITLE OF INVENTION: Cyclokin that Induces Apoptosis
 : FILE REFERENCE: 2835-E
 : CURRENT APPLICATION NUMBER: US/09/825,563
 : CURRENT FILING DATE: 2001-04-02
 : PRIOR APPLICATION NUMBER: 09/320,424
 : PRIOR FILING DATE: 1999-05-26
 : PRIOR APPLICATION NUMBER: 09/190,046
 : PRIOR FILING DATE: 1998-11-10
 : PRIOR APPLICATION NUMBER: 09/048,641
 : PRIOR FILING DATE: 1998-03-26
 : PRIOR APPLICATION NUMBER: 08/670,354
 : PRIOR FILING DATE: 1996-06-25

Query Match	66.8%	Score 988	DB 4	Length 256
Best Local Similarity	78.9%	Pred. No. 4.4e-97		
Matches 194; Conservative	15	Mismatches 13	Indels 24	Gaps 2

```
Search completed: September 5, 2004, 09:27:04
Job time : 18 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:23:01 ; Search time 25 Seconds
(without alignments)
1081.193 Million cell updates/sec

Title: US-10-662-431-2
Perfect score: 1478
Sequence: 1 MAMMEVQGGPSLTGTCVLIV.....NEHLIDMDHRSFPGAFIVG 281

Scoring table: BLAST62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	189.5	12.8	279	2	A53062
2	186	12.6	281	2	I38707
3	177.5	12.0	278	2	A49266
4	164	11.1	261	2	S53090
5	147.5	10.0	261	2	I53476
6	141	9.5	234	1	A25451
7	141	9.5	260	2	S17238
8	134.5	9.1	204	1	S17289
9	133	9.0	232	1	S12606
10	131.5	8.9	233	1	S22052
11	131	8.9	234	1	JQ1344
12	130.5	8.8	233	1	S24642
13	129.5	8.8	235	2	I54490
14	127.5	8.6	204	1	S24641
15	125.5	8.5	233	1	QWJHUN
16	123.5	8.4	235	2	QWMSN
17	123.5	8.4	235	2	JU0029
18	122	8.3	205	1	JH0529
19	121	8.2	234	1	JH0529
20	115.5	7.8	193	2	S06192
21	114	7.7	202	1	B27303
22	113.5	7.7	185	2	S52715
23	113.5	7.7	306	2	I49139
24	112.5	7.6	638	1	QOBY2M
25	111.5	7.5	202	1	JN0869
26	109	7.4	652	2	I48083
27	107	7.2	197	1	JH0309
28	102	6.9	244	2	A46066
29	100	6.8	865	2	AB1658

30	99.5	6.7	233	2	S11688	tumor necrosis fac
31	97.5	6.6	448	2	F95122	protein kinase, pr
32	95	6.4	345	2	T14707	DNA ligase homolog
33	95	6.4	365	2	T15010	hypothetical prote
34	95	6.4	455	2	G95104	hypothetical prote
35	94.5	6.4	4981	2	T18489	hypothetical prote
36	94	6.4	1465	2	T23056	chromodomain helic
37	92.5	6.3	1538	1	A31593	heat shock transcr
38	92.5	6.3	1176	2	JN0583	cardiac muscle fac
39	91	6.2	502	2	A53444	myosin-light-chain
40	90.5	6.1	502	2	JC2491	activin receptor-1
41	90.5	6.1	1284	2	T40578	serine/threonine k
42	90.5	6.1	907	2	B96636	hypothetical prote
43	89.5	6.1	313	2	T03031	NBS-LRR type resis
44	89.5	6.0	328	2	B59296	alpha-N-arabinofur
45	89	6.0				

ALIGNMENTS

RESULT 1

A53062

Fas ligand - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C/Accession: A53062

R/Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nagai

A/Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in t

A/Accession number: A53062; MUID:94185175; PMID:7511063

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-279 <TAK>

A/Cross-references: GB:U06948; MID:9473564; PIDN:AA17800.1; PID:9473565

Query Match

Best Local Similarity 12.8%; Score 189.5; DB 2; Length 279;
Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;

QY	83	QRLQVRKMIILTSETTISTVQEKQONISPLVERGPPQVAAHITGRGRSNTLSPPNSK	142
DB	111	ELREFPTNSL-----KVSSFEKQJANPSTPEKKEPRSV-AHITG-----NPHSR	154
QY	143	NEKALGRKINWESSRSRSHSLNHLNGBELVHEKGFYIYSQTYRFFQBEIKENTYN	202
DB	155	SLPL-----EWEDT-YGTALISGVKKYKGLIVNETGIFYVYSKYVFRGQ-----SCN	201
QY	203	DKQWQYIV-KYTSYDDPILMKSR-NSCWSKDAEYGLYSTYOGIFELKENDRIFVSV	260
DB	202	NQPLNKHXYMNSKKYDEPILVIMEKRLNYCTT--GQIWAHSSYLDVAVENLTASDHLVYNI	259
QY	261	TNEHLIDMDHRSFPGAF	278
DB	260	QSLSHNFEESKTFRGIV	277

RESULT 2

I38707

Fas ligand - human

C/Species: Homo sapiens (man)

C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C/Accession: I38707; J02340; S57565; I38554

R/Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.

A/Title: Human Fas ligand: gene structure, chromosomal location and species specificity.

A/Reference number: I38707; MUID:95127560; PMID:7826947

A/Accession: I38707

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: mRNA

A/Residues: 1-281 <RES>

A/Cross-references: EMBL:U11821; MID:9595430; PIDN:AAC50124.1; PID:9595431

[illegible]

	Query Match	12.0%	Score 177.5;	DB 2;	Length 278;	
	Best Local Similarity	27.5%;	Pred. No. 1.6e-07;			
	Matches	50;	Conservative	39;	Mismatches 64;	Indels 29; Gaps 8;
QY	100	ISTVQKQONISPIVRERGPQRVAAHITGT-RGRSNTLSSEPSNKEKALGKKINSWESSR	158			
Dd	121	VSSREKQANPSTSEPTSETKKPRSV-AHLTGNRRSSIPL-----EWEPT-	162			
QY	159	SGHSFSLNLHRNSELIVHEKGFFYYISQTFRFOEIKENTRKDKQWCXYI-KYTSYP	217			
Dd	163	YGIMLISGVTKKGGGLVYNAGLYFVYSKYVFPRG-----SCNGQLPSHKVMANFKXP	216			
QY	218	DPILLMSAR-NSCWSMDAEYGLYSIIYOGGFELKENDRIEVSYSVNEHLIDMDEASFG	276			
Dd	217	GDLVIMEKKINLYCTT-GQIMWASSYGAVFNLTVADHLVNISQLSLINFESKIIFPG	274			
QY	277	AF 278				
Dd	275	LX 276				

```

RESULT 4
S53090
CD40 ligand - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C/Accession: S53090
R.Mertens, B.E.L.C.; Muriuki, M.
submitted to the EMBL Data Library, February 1995
A/Description: Cloning of bovine Cd40L and homology to bovine TNFA and TNFB.
A/Reference number: S53090
A/Accession: S53090
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-261 <MBR>
A/Cross-references: EMBL:Z48469; NID:G732569; PIDN:CA88363.1; PID:G732570

Query Match
Best Local Similarity 11.1%; Score 164; DB 2; Length 261;
Matches 72; Conservative 52; Mismatches 114; Indels 40; Gaps 14;

QY 6 VGGSELGQTCVLIYFTLL--QSICVAVTYVYFTNEIKOMQDKYSKSGIACFLKEDDS 63
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
D5 13 VATGPVSMK-IFMYLLTFLITOMTGSALFAVYLLHRDLKIDEDKNHEDDFPMK---T 68
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 64 YMDPNEESNMS--PCQVYKQHLQVLKMLITSEITISTVQEKQNTSPVLRGPPOR 121
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
D5 69 IQRCHNGEGSLILNCEHETRSFEDLV-KDIMQNK-----YKKEKNFEMHAKDORPQ- 121
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 122 VAAHITGTRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSN--LHIRNG-ELVIHE 178
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
D5 122 IAAHV-----ISEASGKTSVLT---QW--APKGYTILSNMLVTLENGQALVAKR 165
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 179 KGVYIYSQYFRFOEIKENTKNDKQWQYIKYKTSYPPILMLKSAKNSCWSKDAEYG 238
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
D5 166 QGFYFIYTYVTFCSNRE---TISQAPFIASLCLKSSGGERILIRAAANHSSSKPC--G 219
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 239 LYSIYOGGIFELKENDRIEFSVTNEHLIDMDHSAFPFG 276
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
D5 220 QQSIIHLSGVFELQSGASVFYNVTDPSQVSHGTGTSPG 257
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

RESULT 5
I53476
CD40 ligand - human
N/Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001
C/Accession: S28017; JH0793; S26694; S28852; I53476; S25684; S30593
R.Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.;
EMBO J. 11, 4313-4321, 1992
A>Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for

```

R.Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, T.; Kiyota, T.; Hayashi, H.
DNA 5, 149-156, 1986
A>Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rabbit tumor necrosis factor.
A:Reference number: A25454; MUID:86219711; PMID:3519137
A:Molecule type: mRNA
A:Residues: 1-234 <IT0>
A:Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
R:Ito, H.; Shirai, T.; Yamamoto, S.; Akita, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
DNA 5, 157-165, 1986
A>Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
A:Accession: A25451
A:Molecule type: DNA
A:Residues: 1-234 <IR2>
A>Note: this sequence differs from that shown in having a Gln inserted between residues F:181/Shahov, A.N.; Kuprash, D.V.; Azarov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A>Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF
A:Reference number: JH0309; MUID:91065534; PMID:2249779
A:Accession: J50727
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-62, 'Q', 63-234 <SHA>
A:Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756
C:Genetics:
A:Insertions: 62/3; 80/1; 96/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F:-81/Domains: propeptide #status predicted <PRO>
F:82-234/Product: tumor necrosis factor #status predicted <MAT>
F:9,20/Binding site: myristate (lys) (covalent) #status predicted
F:93/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:147-178/Disulfide bonds: #status predicted

Query Match 9.5%; Score 141; DB 1; Length 234;
Best Local Similarity 22.4%; Pred. No. 0.00016;
Matches 62; Conservative 41; Mismatches 98; Indels 76; Gaps 13;

Dy 8 GGPSLQGTCLVIVTFLVLSLCVAATVYVFETNELKQMOKDKSSGICFLKEDSYMDP 67
 ||| : : : : : |||
Db 22 GGPQGSKRCLCLSTFFFL-----VAGATTTF-----CLL-HRVIGP 58
 ||| : : : : : |||
Dy 68 NDESNNSPCWQYKWQLROLVRMT-LRTSEETISTVOEKQONISPLVRKGPGQVAHHI 126
 :
Db 59 QEESEPN-----LHLVPVQAQWTLLRSASRLSD-----KPL-----AHV 94
 :
Dy 127 TGTGRGSNTLSPNSNGEAKLRKINSWESSRSCHSFTSLNLHNGLVLVIHEKGFYYYS 186
 :
Db 95 VA-----NPVEEQQL-----QMLSQRAALANAMCKLTLDNVLPADGHYLYYS 138
 :
Dy 187 QTFRFOEIKENTKNDKMVGQYIKY-TSPYPILIMKSARNCSWKDAFYG-----LY 240
 :
Db 139 QVLFESGQ-----GCRSVYLITHVSFRFAVSYPEKKWLISAISKCPRETPBEAEPMAYE 193
 :
Dy 241 SIYGGEIFELKENDRIEFSVTNEHLIDMDEAS-FFG 276
 :
Db 194 PVLGGVFLERKDRLETVNQPEYIDLAEISGVYFG 230
 :

RESULT 7
CD40 ligand - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999
C:Accession: S21738
R:Arnltge, R.J.; Panlow, W.C.; Strockbine, L.; Sato, T.A.; Clifford, K.N.; Macduff, B.N.
Nature 357, 80-82, 1992
A>Title: Molecular and biological characterization of a murine ligand for CD40.
A:Reference number: S21738; MUID:92244364; PMID:1374165
A:Molecule type: mRNA

Db 182 EGAAKPMYEPYILGVFQLEKDRLSAEINLPDYIDFAESGQVYFG 228

RESULT 10

22052

tumor necrosis factor alpha precursor - baboon

C/Species: Papio sp. (baboon)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C/Accession: S22052

R:Sanjanwala, M.; Edwards, A. submitted to the EMBL Data Library, September 1991

A/Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.

A/Reference number: S22052

A/Accession: S22052

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-233 <SAN>

A/Cross-References: EMBL:X62141; NID:G38159; PIDN:CAA44068.1; PID:G38160

C/Genetics:

A/Intons: 62/3; 78/1; 94/1

C/Superfamily: tumor necrosis factor

C/Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F:19/20/Binding site: myristate (lys) (covalent) #status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:145-177/Disulfide bonds: #status predicted

Query Match 8.9%; Score 131.5; DB 1; Length 233;

Best Local Similarity 19.2%; Pred. No. 0.001;

Matches 55; Conservative 49; Mismatches 98; Indels 85; Gaps 10;

QY 2 AMMEVGGPSLGQTCVLIVFTVLIQSLCAVATVYVFTNELKQMDKYSKSGIACFLXED 61

Db 16 ALPKTKGGQGSRRCLFLSFLVLAAGTTLFLCHFGVIGQREFFK----- 65

QY 62 DSYWDPNDESNMSPQWQVWKQRLQVLRKMLRTSEETISTVQEKQINSPVRRGPR 121

Db 66 ----DP-----SLISPLAQA-----VSSSRTPS-----DK 87

QY 122 VAAHITGTRGSNTLSSPNSKNEKALGRKINSMESSRSGHSLNHLRNGELVTHEK 181

Db 88 PVAHVVA-----NQAEQGL--QWLNRNALLANGVELRDNDQVLPSEGL 131

QY 182 YTIYSQTYFRFOEIKENTKNDKQWQVITYKYT-----SYDPDILMKSAKNSCWSK-- 233

Db 132 YTIYSQVLFKQ-----GCPSTHVLTHITISRLAVSYPSKVNLSAIKSPCHTE 182

QY 234 ---DAEYGIYISQTYFRFOEIKENTKNDKQWQVITYKYT-----SYDPDILMKSAKNSCWSK-- 276

Db 183 EGAAKPMYEPYILGVFQLEKDRLSAEINLPDYIDFAESGQVYFG 229

RESULT 11

201344

tumor necrosis factor alpha precursor - horse

N/Alternate names: cachectin; TNF alpha

C/Species: Equus caballus (domestic horse)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C/Accession: J01344

R:Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A/Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis f

A/Reference number: J01344; MUID:92084125; PMID:1748301

A/Accession: J01344

A/Molecule type: DNA

A/Residues: 1-234 <STX>

A/Cross-References: GB:M64087; NID:G164244; PIDN:AAA30959.1; PID:G164245

C/Comment: This protein is an important proximal mediator of endotoxemia.

C/Genetics:

A/Gene: TNF-alpha

A/Intons: 62/3; 79/1; 95/1

C/Superfamily: tumor necrosis factor

C/Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; mem

F:78-234/Product: tumor necrosis factor alpha #status predicted <TNX>

F:19/20/Binding site: myristate (lys) (covalent) #status predicted

F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:146-178/Disulfide bonds: #status predicted

Query Match 8.9%; Score 131; DB 1; Length 234;

Best Local Similarity 20.8%; Pred. No. 0.0011;

Matches 60; Conservative 40; Mismatches 89; Indels 100; Gaps 13;

QY 8 GGPSLGQTCVLIVFTVLIQSLCAVATVYVFTNELKQMDKYSKSGIACFL-----K 59

Db 22 GGPGSRRCLCLFSFL-----VAGATTLF-----CLHFGVIGRGP 60

QY 60 EDDSYWDPNDESNMSPQWQVWKQRLQVLRKMLRTSEETISTVQEKQINSPVRRGPR 119

Db 61 EEOGL---PNAFQGIN-PLAQT-----LRSSSRTPS----- 86

QY 120 QRAVAHITGTRGSNTLSSPNSKNEKALGRKINSMESSRSGHSLNHLRNGELVTHEK 179

Db 87 DKPAHVVA-----NQAEQGL--QWLNRNALLANGVELRDNDQVLPSEGL 130

QY 180 GFYIYSQTYFRFOEIKENTKNDKQWQVITYKYT-----SYDPDILMKSAKNSCWSK 233

Db 131 GLYIISQVLFKQ-----GCPSTHVLTHITISRLAVSYPSKVNLSAIKSPCHTE 181

QY 234 DAEYG-----LYSIYOGIIFELKENDRIEVSVTNEHLIDMDHEAS-FFG 276

Db 182 SPQAAKPMYEPYILGVFQLEKDRLSAEINLPDYIDFAESGQVYFG 230

RESULT 12

S24642

tumor necrosis factor alpha precursor - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C/Accession: I46047; S24642

R:Cluets, T.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.

Cyokine 5, 336-341, 1993

A/Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tun

A/Reference number: I46046; MUID:94083525; PMID:8260599

A/Accession: I46047

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-233 <CL2>

A/Cross-References: EMBL:214137; NID:G796; PIDN:CAA78511.1; PID:G798

C/Genetics:

A/Gene: TNFA

A/Intons: 62/3; 78/1; 94/1

C/Superfamily: tumor necrosis factor

C/Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F:20/Binding site: myristate (lys) (covalent) #status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:145-177/Disulfide bonds: #status predicted

Query Match 8.8%; Score 130.5; DB 1; Length 233;

Best Local Similarity 20.3%; Pred. No. 0.0013;

Matches 59; Conservative 43; Mismatches 95; Indels 93; Gaps 13;

QY 3 MMEVGGPSLGQTCVLIVFTVLIQSLCAVATVYVFTNELKQMDKYSKSGIACFL----- 58

Db 17 LSEKAGGQGSRRCLCLFSFL-----VAGATTLF-----CLHFGV 55

QY 59 ---KEDSYWDPNDESNMSPQWQVWKQRLQVLRKMLRTSEETISTVQEKQINSPVRRGPR 115

Db 56 IGPREBSPGP-----SINSPVLT-----LRSSSQAS-- 85

QY 116 ERGQRAVAHITGTRGSNTLSSPNSKNEKALGRKINSMESSRSGHSLNHLRNGELV 175

Db 86 ---NKPAHVVA-----DINSPQGR-----WMDSYANALMANVAKLEDNQLV 125

QY 176 IHEKGFYIYSQTYFRFOEIKENTKNDKQWQVITYKYT-----SYDPDILMKSAKNSC-- 230

Db 126 VPADGLYIISQVLFKQ-----GCPSTHVLTHITISRLAVSYOTKVNLSAIKSPCHRE 180

QY 231 ---MSKDAEGLYSITOGGIFELKENDRIFSVTNEHLIDMDHEAS -FFG 276
 Db 181 TPMAA-EAAKPMYEPITOGGVFQLEKGRLSAEINLPDYLYAESGVYFPG 229
 RESULT 13
 154490
 tumor necrosis factor alpha precursor - white-footed mouse
 C/Species: Peromyscus leucopus (white-footed mouse)
 C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
 C/Accession: 154490
 R/Crew: M.D., Filipowsky, M.E.
 Immunogenetics 35, 351-353, 1992
 A/Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leu
 A/Reference number: 154490; PMID:92218012; PMID:134497
 A/Accession: 154490
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-235 <RES>
 C/Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507
 C/Genetics:
 A:Gene: PLTNF
 A:Introns: 62/3; 81/1; 97/1
 C:Superfamily: tumor necrosis factor
 C/Keywords: glycoprotein, lipoprotein, myristylation
 F/19,20/Binding site: myristate (Lys) (covalent) #status predicted
 F/84/Binding site: carbohydrate (Ser) (covalent) #status predicted
 Query Match 8.8%; Score 129.5; DB 2; Length 235;
 Best Local Similarity 24.5%; Pred. No. 0.0015;
 Matches 45; Conservative 39; Mismatches 75; Indels 25; Gaps 9;
 QY 110 ISPLVRERGPQVAAHITGTRGRSNTL-SSPNSKNEKALGRKINGWE-----SSRSCH 161
 Db 56 IGPQEEKPPNMLP--IIQMAQTLLIRSSSQNSDPVAVVAVHQQVDEQLEWLSRGAN 113
 QY 162 SFLSN-LHNRNDELVHEKGFYIYSQTFERFOBEIKENTKDKQWQVQIYKY-TSPDP 219
 Db 114 ALLANGMDIKDQVLIPADGLVYSQVLPKQ-----GSSVVLITHVVSFANYSDEK 168
 QY 220 IILMSARNSCMSKDAEY-----LYSITOGGIFELKENDRIFSVTNEHLIDMDHEAS 273
 Db 163 VALLSLKRPCC-PKEIPESSELPKWPETIYLGCVFQLEKGRLSARVNP.KYLDFAESGQ 227
 QY 274 -FFG 276
 Db 228 VYFPG 231
 RESULT 14
 S24641
 lymphotoxin - bovine
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: I46046; S24641
 R/Citrus, T., Clauter, Y., Kettman, R.; Burny, A.; Droogmans, L.
 Cytokine 5, 336-341, 1993
 A/Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tu
 A/Reference number: I46046; PMID:94083525; PMID:8260599
 A/Accession: I46046
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-204 <CL2>
 A/Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78510.1; PID:g797
 C/Genetics:
 A:Introns: 32/3; 68/1
 C:Superfamily: tumor necrosis factor
 Query Match 8.6%; Score 127.5; DB 1; Length 204;
 Best Local Similarity 24.9%; Pred. No. 0.0019;
 Matches 47; Conservative 29; Mismatches 78; Indels 35; Gaps 9;
 QY 99 TISIVGKQONISPLVRERGPVAAHITG-----TRGRSNTLSSPNSKNEKALGRKI 151

Db 40 TPBAQPAHQOL-PTPFTRGTLKPAALVGDPTQDSLRRPANT-----DRAFLR-- 88
 QY 152 NSMSESSSGHSFLSNLHNRNGELVHEKGFYIYSQTFERFOBEIKENTKDKQWQVQIY 211
 Db 89 -----HGF-----SLSNSLIVPTSGILFYVSQVVFSGRGCPRRATPPLVLAHVQ 135
 QY 212 KYT-SYDPPILMKSARNSCMSKDAEGLYSITOGGIFELKENDRIFSVTN-ETHLMD 269
 Db 136 LFSQYQFHHVPLLSAQSGVCPGQGPW-VRSVYQGAFFLLTRGDQLSTHTDGIHLL-LS 193
 QY 270 HEASFFGAF 278
 Db 194 PSSVFFGAF 202
 RESULT 15
 OMHUN
 tumor necrosis factor alpha precursor [validated] - human
 N/Alternate names: cachectin; TNFA
 C/Species: Homo sapiens (man)
 C/Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000
 C/Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23;
 R/Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.
 Nucleic Acids Res. 13, 6361-6373, 1985
 A/Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chro
 A/Reference number: A93585; PMID:86016093; PMID:2995927
 A/Accession: A93585
 A/Molecule type: DNA
 A/Residues: 1-233 <NED>
 A/Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
 R/Itte, F.J.M.; Bougueleret, L.; Prieux, S.; Caterina, D.; Primas, G.; Perrot, V.; Jutka,
 Nature Genet. 3, 137-145, 1993
 A/Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
 A/Reference number: S36153; PMID:93272029; PMID:8499947
 A/Accession: S36153
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-233 <IRI>
 A/Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
 R/Pennica, D.; Nedwin, G.E.; Haylick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.;
 Nature 312, 724-729, 1984
 A/Title: Human tumor necrosis factor: precursor structure, expression and homology to 1)
 A/Reference number: A93351; PMID:85086244; PMID:6392892
 A/Accession: A93351
 A/Molecule type: mRNA
 A/Residues: 1-233 <PBN>
 A/Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
 A/Note: this protein was isolated from the monocytic-like cell line HL-60 from a promyeloc
 R/Wang, A.M.; Creasey, A.A.; Ladher, M.B.; Lin, L.S.; Strickler, J.; Van Arsdale, J.N.;)
 Science 228, 149-154, 1985
 A/Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
 A/Reference number: A44189; PMID:85142190; PMID:3856324
 A/Accession: A44189
 A/Molecule type: mRNA
 A/Residues: 1-62, 'S', 64-233 <MAN>
 A/Cross-references: GB:M10988; NID:g39737; PIDN:AAA61198.1; PID:g39738
 R/Rukuda, S.; Ando, S.; Sanou, O.; Tanial, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; Aoc
 Lymphokine Res. 7, 175-185, 1988
 A/Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
 A/Reference number: A61478; PMID:88301617; PMID:2641543
 A/Accession: B61478
 A/Molecule type: protein
 A/Residues: 83-102;109-119;121-128,'X',130-131,142-144,'X',146,'XXX',150-152,159-174,180,
 R/Marmenout, A.; Franssen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima, I
 Eur. J. Biochem. 152, 515-522, 1985
 A/Title: Molecular cloning and expression of human tumor necrosis factor and comparison v
 A/Reference number: I53311; PMID:8603026; PMID:3932069
 A/Accession: I53311
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-233 <MAR>

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:20:06 : Search time 62 Seconds

(Without alignments)
1430.010 Million cell updates/sec

Title: US-10-662-431-2
Sequence: 1478

Scoring table: 1 MAMMEVGGPSLQGTCLIV.....NEHLIDMREASFGALVIG 281

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_orcanelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	963	65.2	287	11	Q8K3G0
2	809.5	54.8	304	13	Q7L1F2
3	334.5	32.6	317	13	Q7ZYX9
4	307.5	20.8	287	13	Q9WTF9
5	305.5	20.7	214	13	Q9DDZ5
6	184.5	12.5	279	11	Q7WTV9
7	180	12.2	252	11	Q8K3Y8
8	178.5	12.1	280	6	Q8K1W5
9	175.5	11.9	169	11	Q9WV90
10	175	11.8	252	11	Q8OYZ0
11	173	11.7	252	4	Q8K3Y7
12	166	11.2	251	4	Q8WTF9
13	157	10.6	154	6	Q8K1W5
14	153.5	10.4	227	13	Q7L1F2
15	144.5	9.8	216	11	Q7O3J2
16	141	9.5	231	13	Q8AW02

17	137.5	9.3	232	11	Q80XA4	Q80XA4 peromyscus
18	135	9.1	156	11	Q91ZL4	Q91ZL4 sigmodon hi
19	135	9.1	215	6	Q9BER8	Q9BER8 erinaceus e
20	135	9.1	217	11	Q9ERG6	Q9ERG6 peromyscus
21	130.5	8.8	222	13	Q7T1U4	Q7T1U4 pagrus majo
22	130.5	8.8	225	13	Q91B41	Q91B41 paralichth
23	130.5	8.8	225	13	Q91B42	Q91B42 paralichth
24	128	8.7	230	13	Q8UG37	Q8UG37 ictalurus p
25	127	8.6	253	13	Q7T1U4	Q7T1U4 acanthopagr
26	126.5	8.6	215	11	Q99ND1	Q99ND1 tamiasciuru
27	124	8.4	216	6	Q9BEC4	Q9BEC4 talpa europ
28	123.5	8.4	205	6	Q9BEC9	Q9BEC9 ochotona pr
29	122	8.3	216	6	Q9BEC9	Q9BEC9 ochotona pr
30	121.5	8.2	246	13	Q8N4C3	Q8N4C3 homo sapien
31	121.5	8.2	246	13	Q91976	Q91976 oncorhynch
32	120	8.1	237	13	Q8AWC9	Q8AWC9 cyprinus ca
33	119	8.1	232	11	Q80WE7	Q80WE7 peromyscus
34	116.5	7.9	217	6	Q9BER0	Q9BER0 cyclopes di
35	116.5	7.9	217	6	Q9BER4	Q9BER4 cabassous u
36	115.5	7.8	149	6	Q97543	Q97543 salvelinus
37	113.5	7.7	255	13	Q91810	Q91810 oncorhynch
38	113.5	7.7	255	13	Q9DEP9	Q9DEP9 oncorhynch
39	112.5	7.6	217	6	Q9BER1	Q9BER1 bradypus tr
40	112.5	7.6	638	8	Q9Z2W6	Q9Z2W6 saccharomyc
41	110	7.4	93	6	Q9T1U2	Q9T1U2 bos taurus
42	109.5	7.4	149	6	Q97538	Q97538 actus vocif
43	109.5	7.4	149	6	Q97T88	Q97T88 actus nigri
44	109	7.4	288	13	Q8JHJ4	Q8JHJ4 gallus gall
45	109	7.4	652	11	Q60421	Q60421 cricetus

ALIGNMENTS

RESULT 1

Q8K3G0 ID Q8K3G0 PRELIMINARY; PRT; 287 AA.
AC Q8K3G0;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE TNF-related apoptosis inducing ligand.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DA;
RA Mueller A.M., Giegerich G.;
RT "Rattus norvegicus TNF-related apoptosis inducing ligand (TRAIL).";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBS databases.
DR EMBL; AY115578; AA049797.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF-like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00251; TNF; 1.
DR PROSITE; PS00251; TNF; 1.
DR PROSITE; PS0049; TNF; 2; 1.
SQ SEQUENCE 287 AA; 32979 MW; CAAF5B5D7C833FEC CRC64;

Query Match 65.2%; Score 963; DB 11; Length 287;
Best Local Similarity 67.7%; Pred. No. 2.7e-72;

Matches 189; Conservative 29; Mismatches 51; Indels 10; Gaps 3;

QY 9 GPSLGG-----TCVLIIVFTVLQSLCAVTVTVFTEINLKQMDKSKSGICGLKEDSDY 64
DB 9 GPSFSQHTMTVICIVLQVLLQALTVAVTYMYENNEVKQIDMYSKIGLACFSKEDSDIF 68

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QY 65 WDNDEBSMNSPCQVQKQOLRQVLRKMLRTSEETISTVQKQONISPLVREBQGVAA 124
DB 69 WDSDEGLINPFCQVQKQOLRQVLRKMLRTSEETISTVQKQONISPLVREBQGVAA 128
QY 125 HITRGRSNTLSSPNSKNEKALGRKINSWSSRGSHFSLNHLRNGELVHHEKGFYI 184
DB 129 HITGTRRSNALIPISKDGKTLQKLETWSSRGSHFSLNHLRNGELVHHEKGFYI 188
QY 185 YSQTYFRPQE--EIKENTKND---KQWQYIYKTYSPDPILMKASRNSCWDAYG 238
DB 189 YSQTYFRPQE--EIKENTKND---KQWQYIYKTYSPDPILMKASRNSCWDAYG 248
QY 239 LYSIYQGGIFELKENDRIFVSVTNHLLDMDEHASFPGA 277
DB 249 LYSIYQGGIFELKENDRIFVSVTNHLLDMDEHASFPGA 287

RESULT 2
Q7T1F2 PRELIMINARY; PRT; 304 AA.
AC 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE Tumor necrosis factor related apoptosis inducing ligand.
GN Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP TISSUE=Spleen;
RA Horiuchi H.H., Furusawa S., Matsuda H.;
RT "Identification and Characterization of Chicken TNF-Superfamily
RT Ligand 8 (CD30 Ligand) and 10 (Tumor Necrosis Factor Related Apoptosis
RT Inducing Ligand (TRAIL).";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB114678; BAC79267.1; -.
SQ SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;

Query Match 54.8%; Score 809.5; DB 13; Length 304;
Best Local Similarity 55.4%; Pred. No. 1.9e-59;
Matches 160; Conservative 45; Mismatches 65; Indels 19; Gaps 6;

QY 8 GGSILGQTCVLIVFTVLLQSLCAVATYYVFTNELKQMDKYSKSGIACFLKEDSYWDP 67
DB 5 GGSFPAHTGCAVLVAVALIQSVCAVATYYVFTNELKQMDKYSKSGIACFLKEDSYWDP 64
QY 68 N-----DEBSMNSPCQVQKQOLRQVLRKMLRTSEETISTVQ--EKQONISPLVREBQ 120
DB 65 NLDVSEKSRVADPCQVQKQOLRQVLRKMLRTSEETISTVQ--EKQONISPLVREBQ 122
QY 121 ---RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWSSRGSHFSLNHLRNGELVH 177
DB 123 PTLRIAAHLGSSKRSA--SPHNYLIRGIGLHSHSSRGSHFSLNHLRNGELVH 181
QY 178 EKGFYIYQTYFRPQE-----IKENTKNDKQWQYIYKTYSPDPILMKASRNSC 231
DB 182 QIGGFYIYQTYFRPQRENEDESGLEIRIKNPQOLVQYIKLTNPDPILMKASRNSC 241
QY 232 SKDAEGLYSIYQGGIFELKENDRIFVSVTNHLLDMDEHASFPGA 280
DB 242 SKDAEGLYSIYQGGIFELKENDRIFVSVTNHLLDMDEHASFPGA 290

RESULT 3
Q7ZYX9 PRELIMINARY; PRT; 317 AA.
AC 01-JUN-2003 (TREMBlrel. 24, Created)

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DT 01-JUN-2003 (TREMBlrel. 24, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE Similar to tumor necrosis factor (ligand) superfamily, member 10.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044336; AA044336.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD02012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS0049; TNF 2; 1.
SQ SEQUENCE 317 AA; 35465 MW; 68F76BC1A40DCE9F CRC64;

Query Match 22.6%; Score 334.5; DB 13; Length 317;
Best Local Similarity 29.2%; Pred. No. 8.7e-20;
Matches 83; Conservative 55; Mismatches 113; Indels 33; Gaps 8;

QY 18 LIVITVLLQSLCAVATYYVFTNELKQMDKYSKSGICF-----LKEDSYWDPND--EE 71
DB 40 MWIVVAVVQLASTGLVTLNMSLSQVSGVTLEKLGILNVLGKQDI--FEDLAQ 97
QY 72 SMNSPCQVQKQOLRQVLRKMLRTSEETISTVQKQONISPLVREBQ 120
DB 98 LFGEKMLKASIGKAVISKVDSIISKQTLHARTRTHSYNTGSKFMVTV-----MQ 150
QY 121 RVAAHITGTRGSRNT-----LSSPNSKNEKALGRKINSWSSRGSHFSLNHLRNGELV 175
DB 151 RPSAHLTLSSASDNRSPQSDMHQPOFDLHQSGRHVRHW--ANKSGAHLNMTLTNGRLR 209
QY 176 HEKGFYIYQTYFRF--GEIKENTKNDKQWQYIYKTYSPDPILMKASRNSC 234
DB 210 VQDGRYIYQTYFRFPPSPSDQSSVSHQVLCYKTSYINPQLKGVCTKQAPD 269
QY 235 AEYGLYSIYQGGIFELKENDRIFVSVTNHLLDMDEHASFPGA 278
DB 270 AEYGLYSIYQGGIFELKENDRIFVSVTNHLLDMDEHASFPGA 313

RESULT 4
Q9QWT9 PRELIMINARY; PRT; 287 AA.
AC 09QWT9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE TNF-related apoptosis inducing ligand.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "TNF-related apoptosis inducing ligand (TRAIL) expression in the hen
RT ovary.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057941; AL23702.1; -.
DR HSSP; O35235; IIOA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

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Query Match	20.8%;	Score 307.5;	DB 13;	Length 287;
Best Local Similarity	32.3%;	Pred. No. 1.4e-17;		
Matches 93;	Conservative 46;	Mismatches 110;	Indels 39;	Gaps 11.

RESULT 5		
Q9DDZ5		
ID	Q9DDZ5	PRELIMINARY;
AC	Q9DDZ5;	PRT; 214 AA.
DT	01-MAR-2001 (TrEMBLrel. 16, Created)	
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	TFAIL-like protein.	
GN	TNFSF10L.	
OS	Brachydanio rerio (Zebrafish) (Danio rerio).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes	
OC	Cyprinidae; Danio.	
OX	NCBI_TaxID=7955;	

[illegible]

Query Match 20.7%; Score 305.5; DB 13; Length 214;

RESULT	6			
Q7TMV9				
ID	Q7TMV9	PRELIMINARY;	PRT;	279 AA.
AC	Q7TMV9			
DT	01-OCT-2003	(TREMBLrel. 25, Created)		
DT	01-OCT-2003	(TREMBLrel. 25, Last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
DE	Tnfisf6 protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
OX	NCBI_TaxID=10090;			

SEQUENCE FROM N.A.
STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
MEDLINE=22388257; Pubmed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Boone K.H., Schaefer C.F., Bat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Siepterson M., Soares M.B., Bonaldo M.F., Cacaavnt T.L., Scheetz T.E.,
Brownstein M.J., Usdn T.B., Toshiyuki S., Carninci P., Prange C.,
Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
Bosak S.A., Mcowan P.J., McKernan K.J., Malek J.A., Gumatre P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
Faley J., Helton E., Kettlem M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.J., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyniowski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Matta M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
EMBL: BC052866, AAH52866.1, --
CQ
SEQUENCE 279 AA; 31416 MW; C297252728FBBB7B CRC64;

Query Match	12.5%;	Score 184.5;	DB 11;	Length 279;
Best Local Similarity	25.3%;	Pred. No. 2.4e-07;		
Matches 50; Conservative	51;	Mismatches 64;	Indels 33;	Gaps 9;

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OY      83  QURQYKMLIRLISEETITVOEQOQIMSPILVRGRGQPVAAHTGTGRNTSLSPMSK 142
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      111  ELREFPTQSL-----KVSPFEKQIAMPSTSEKKEPRSV-AHTG-----NPHSR 154
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      143  NEKALGKINSMESSRSGHSLSLHLHNGELVHERGEFYIYSQTPRQPEIKENKRN 202
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      155  SLP-----EMEDT-YGTALISGVKKKGGALVNETGVLVYSKVYFRGQ-----SCN 201
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      203  DKQWQYTY-KYTSYDPDILIMSGAR-NSCMSKDAEYGLVSIYOGGIFELKENDRIFVSV 260
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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OX NCBI_TaxID=9995;
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20010026; PubMed=10540161;
RA Hodgson P.D., Grant M.D., Michalak T.L.;
RT "Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and
RT chronic woodchuck viral hepatitis.";
RL Clin. Exp. Immunol. 118:63-70(1999).
DR EMBL; AF152368; AAD38387.1; -.
DR HSPSP; P50591; ID4V.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR009883; TNF-like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 169 AA; 19274 MW; FDE395B014717B6B CRC64;

Query Match 11.9%; Score 175.5; DB 11; Length 169;
Best Local Similarity 27.8%; Pred. No. 7.2e-07;
Matches 54; Conservative 39; Mismatches 58; Indels 43; Gaps 10;

QY 83 QLRQVAKMLIRSEETISVQEKQONISPLVERGQRYVAHITGRGNSNTLSPNSK 142
DB 10 ELRESINQ--RTEPSL-----EKQIGHSPSPDKALRAAHIT--GPNRSRP--- 56
QY 143 NEKALRKTKINSWESSRSGHSFLSN-LHLNGLVYHEKGFYIYSQTYFRPQEI 202
DB 57 -----LEWEDT-YGISLISGVKVKQKGLVINDTGLFYVSKTYFRGQ-----SCN 100
QY 203 DKQWQYIY-KYTSYDPIILMK-SARNSC-----MSKDAEYGLYSIYQGGIFELKENDR 255
DB 101 NQPLSHKVVYKSKYQDVLWEGKXMYCTTGQMMAR-----SSYLGAVNFYNTSDH 153
QY 256 IFVSVTNEHLIDMD 269
DB 154 LYVNVSELSLINE 167

RESULT 10
Q80YZO PRELIMINARY; PRT; 252 AA.
AC Q80YZO;
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-OCT-2003 (TREMblrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE BM20K13.3 (Tumor necrosis factor (Ligand) superfamily, member 15).
GN TNFSF15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AL691468; CAD83021.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

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DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNFCROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 252 AA; 27725 MW; A63ABDC9B969EDF CRC64;

Query Match 11.8%; Score 175; DB 11; Length 252;
Best Local Similarity 31.9%; Pred. No. 1.3e-06;
Matches 68; Conservative 26; Mismatches 81; Indels 38; Gaps 12;

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QY 83 QLRQVAKMLIRSEETISVQEKQONISPLVERGQRYVAHITGRGNSNTLSPNSK 142
DB 63 QLRVPGDKMLRAITERSE-PSPOQVYSP---PRGKFR--AHIT-----IKQTPADHLK 112
QY 143 NE-KALGRKINSWESSRSGHSFLSN-LHLNGLVYHEKGFYIYSQTYFRPQEI----- 196
DB 113 NQLSAL-----HWEHD-LGMAFTKNGKTYKSLVPESDGYFIYSQITFRGTTVCGDI 166
QY 197 --KENTKDKQWQYIYKYTSYDPIILMKASARNSC-----MSKDAEYGLYSIYQGGIF 248
DB 167 SRGRPRPKPDSITMTVITKVAQSYEPAPRLITGSKVCELSNNM-----FQSLYLGAITF 219
QY 249 ELKENDRIPVSVTNEHLIDMDHE-ASFPGAFV 280
DB 220 STEEGRLMVNVSDISLVYTKEDKTFPGAFL 252

RESULT 11
Q8K3Y7 PRELIMINARY; PRT; 252 AA.
AC Q8K3Y7;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE TNF superfamily ligand TL1A.
GN TNFSF15.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21909416; PubMed=11911831;
RA Mlgone T.S., Zhang J., Luo X., Zhuang J., Chen C., Hu B., Hong J.S.,
RA Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,
RA Carrell J., Boyd E., Olsen H.S., Hu G., Fukac L., Liu D., Ni J.,
RA Kim S., Gentz R., Feng P., Moore P.A., Ruben S.W., Wei P.;
RT "TL1A is a TNF-like ligand for DR3 and TR6/DR3 and functions as a T
RT cell costimulator.";
RL Immunity 16:479-492(2002).
DR EMBL; AF520787; AAM77368.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNFCROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 252 AA; 28029 MW; 7789B6556D46F293 CRC64;

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Query Match 11.7%; Score 173; DB 11; Length 252;

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Best Local Similarity 32.7%; Pred. No. 1.9e-06;
Matches 56; Conservative 23; Mismatches 62; Indels 30; Gaps 8;

QY 124 AHITGRGRSNTLSSPNSKNEKALGRKINSWSSSGHSFLSN-LHLNGLVHEKGFY 182
DB 98 AHLTMR-----QTPVPHKNELA-----ALHWNEN-LGNAFTKRNRYNFKFLVIPSADY 148
QY 183 YIYSGTYRFPQ-----EIKENKNDKQWQYIYKTSYDPLILKMSARNSC----- 230
DB 149 FYSQITRGTSTSECGDISRVRPRKPSITVITKVDSPPEPHLLTGTSVCETISSN 208
QY 231 WSKDAEYGVSYIYOGGIFELKENDRIFVSVTNEHLIDMDHF-ASFFGAFLV 280
DB 209 W-----FQPIYLGAMFSLSEGDILMNVDISLVDYTKELKTFGGAFLI 252

RESULT 12

Q8NFE9 PRELIMINARY; PRT; 251 AA.

AC Q8NFE9; 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE TNF superfamily ligand TLIA.
GN TNFSF15.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=21909416; PubMed=11911831;
RA Migone T.S., Zhang J., Luo X., Zhang L., Chen C., Hu B., Hong J.S.,
Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakara P.,
Carrell J.F., Boyd E., Olsen H.S., Hu G., Fukac L., Liu D., Ni J.,
Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.,
RT "TLIA is a TNF-like ligand for DR3 and TR6/DeR3 and functions as a T
cell costimulator.";
RT Immunity 16:479-492(2002).
RL EMBL; AF520785; AAM77366.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 251 AA; 28087 MW; 65ED70E367E3446D CRC64;

Query Match 11.2%; Score 166; DB 4; Length 251;

Best Local Similarity 33.2%; Pred. No. 7.4e-06;
Matches 62; Conservative 30; Mismatches 65; Indels 30; Gaps 12;

QY 107 QONISPLVBERGQRYVAHITGRGRSNTLSSPNSKNE-KALGRKINSWSSSGHSFLS 165
DB 82 QQYVAELRADGDKPR-AHILTVR-----QTPQHFKNQFPAL-----HMS-HELGLAFK 129
QY 166 N-LHLNGLVHEKGFYIYSGTYRFPQ-----EIKENKNDK-QMWQYIYKYT-SYP 217
DB 130 NRYNYTNKFLIPESGDYFIYSGTYRGTSTSECGDISRVRPRKPSITVITKVDSP 189
QY 218 DPLILKMSARNSCWSKDAEYGV---LYSIYOGGIFELKENDRIFVSVTNEHLIDMDHF-AS 273
DB 190 EPIQOLIMGTGSVC-----EVGSMWPGQPIYLGAMFSLSEGDILMNVDISLVDYTKEDKT 244
QY 274 FFGAFLV 280
DB 245 FFGAFLI 251

RESULT 13

Q8MU19 PRELIMINARY; PRT; 154 AA.

AC Q8MU19; 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fas ligand CD178 (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Petit F., Arnould D., Lelievre J.-D., Lecossier D., Hance A.J.,
RA Monceaux V., Ho Tsong Fang R., Hurtrel B., Ameisen J.-C.,
RA Estaguer J.,
RT "Caspase-dependent and -independent cell death pathways characterize
pathogenic Simian Immunodeficiency Virus infection. Relationship with
disease evolution.";
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF530076; AAM95636.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008064; Fas_ligand.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR PRODOM; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 154
SQ SEQUENCE 154 AA; 17410 MW; 971A43779B029449 CRC64;

Query Match 10.6%; Score 157; DB 6; Length 154;

Best Local Similarity 27.4%; Pred. No. 2.2e-05;
Matches 46; Conservative 33; Mismatches 65; Indels 24; Gaps 6;

QY 95 TSEETISTVQEQONISPLVBERGQRYVAHITGRGRSNTLSSPNSKNEKALGRKINSW 154
DB 8 TSGKHTASLEKQIGHSPPEKEQRKVAHLTG-----KPSRSKWPL-----EW 52
QY 155 ESSRSRSHSLNHLNGLVHEKGFYIYSGTYRFPQEIENKNDKQWQYI-KY 213
DB 53 EPI-VYIVLLSGVKKYKGLVINETGLVYISVYRQ-----SCTNPLSHKYYMRY 105
QY 214 TSYDPLILKMSARNSCWSKDAEYGVLYSIYOGGIFELKENDRIFVSVT 261
DB 106 SKTPQDLVWMEGKMS-YCTTGQMAHSSYLGAVFNLTSADHLHYVNV 152

RESULT 14

Q7T203 PRELIMINARY; PRT; 227 AA.

AC Q7T203; 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Tumor necrosis factor-3 alpha.
GN TNF-3ALPHA.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head Kidney;
 RA Savan R., Sakai M.;
 RT "Cloning of tumor necrosis factor 3 alpha in carp";
 RI Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB112424; BAC77690.1;
 SQ SEQUENCE 227 AA; 25226 MW; 010BC2B1E8D7265E CRC64;

Query Match 10.4%; Score 153.5; DB 13; Length 227;
 Best Local Similarity 20.1%; Pred. No. 7.2e-05;
 Matches 60; Conservative 50; Mismatches 92; Indels 97; Gaps 11;

QY 3 MMEYQGGP-----SIGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKYSK 51
 Db 1 MMDLESQPLFQEWMSRRNASSKSAVWVCGVLLAVLCAAAACFTLAK----- 50
 QY 52 SGIACFLEKDDSYNDPDEESMNSPCWQVAKQQLFQIVRKMLTSEETISTVOEKQONIS 111
 Db 51 -----NNQEGNF-----QRLTLKDN----- 66
 QY 112 PLVREKGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSMESSRSGHSPLSLHLRN 171
 Db 67 -LSKENVTSKVAHLTSGA-----YEDVSKNNIDWKQNDGAFVSGGLKLVLD 112
 QY 172 GEIVTHEKGYIYSQTYFRFQSEIKENTNDKQWQIYKYTSYD-----PILMKKS 225
 Db 113 REIILIPNDGIYFYISQVSEFHI--SKNDMTEDQEVHVSAPVHYSDFGIIYKP--LIRA 168
 QY 226 ARNSCW----SKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF 278
 Db 169 ARSACVHASNTEDVWYD--TTLGAAFSLRAGDKLCTKTTELLPVEVDNNAKTFPGVF 225

RESULT 15
 070332

ID 070332 PRELIMINARY; PRT; 216 AA.

AC 070332;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
 DE Tumor necrosis factor-alpha (Fragment).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA MEDLINE=98234044; PubMed=9573100;
 RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
 RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
 RT analysis of cytokine mRNA expression in experimental visceral
 RT leishmaniasis";
 RI Infect. Immun. 66:2135-2142(1998).
 DR EMBL; AF046215; AAC40100.1; --
 DR HSSP; P06804; 2TNF.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR006053; TNF_adc.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_1like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PRO1234; TNECROSISFCT.
 DR Prodom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.

DR PROSITE; PS50049; TNF 2; 1.
 FT NON TER 1
 FT NON TER 216
 SQ SEQUENCE 216 AA; 23793 MW; BADAE3FB3F45B533 CRC64;

Query Match 9.8%; Score 144.5; DB 11; Length 216;
 Best Local Similarity 26.9%; Pred. No. 0.00038;
 Matches 47; Conservative 26; Mismatches 63; Indels 37; Gaps 7;

QY 118 GPQVAAH---ITGTRGRSNTL--SSPNSKNEKALGRKINS-----MESSRSGHSPLS 165
 Db 49 GPQREKFPNPDIIGSMQTLTLRSSQNSNDKPVGVAAHNVQVEQLEMLSHRANALLAN 108
 QY 166 NLHLRNGELVTHEKGYIYSQTYFRFQSEIKENTNDKQWQIYK-----YTSYD 218
 Db 109 GMSLKNDQVITPADGLYIVTSQVIFRQ-----GCFSVLLTHTVSRIVASVED 157
 QY 219 PILMKSAARNSCWSKDAEYG-----LVSYYGGIFELKENDRIFVSVTNEHLID 267
 Db 158 NVNLLSAIKSPC-PKETPEGEELKPWYEPYLGQVQLKGDHLASAVNLPKYID 211

Search completed: September 5, 2004, 09:26:11
 Job time : 64 secs

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DR N-PSDB; AAT72796.

PT Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce
 PT apoptosis for the treatment of breast and colon cancer.

PS Claim 4; Fig 1a; 72pp; English.

CC A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian
 CC cell apoptosis. It is believed to be a member of the tumour necrosis
 CC factor cytokine family. Its amino acid sequence was deduced from a cDNA
 CC clone (AA172796) isolated from a human placental CDNA library. Apo-2
 CC ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-
 CC 281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells
 CC transformed or transfected with a vector contg. Apo-2 ligand nucleic
 CC acid. They can be used to induce apoptosis in mammals and to treat
 CC pathological conditions such as cancer (esp. breast or colon cancer) or
 CC to raise antibodies useful in diagnostic assays

CC Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MAMMEVGGPSLIGQTCVLIVITFTVLLQSLCAVTVYVTFNKLKQMDKXSKGICFLKE 60
 QY 61 DSDYDNDDESMNSPCWQVQKQLRQVVKMLRTSEETISVQEQONISPLVERGPG 120
 DB 61 DSDYDNDDESMNSPCWQVQKQLRQVVKMLRTSEETISVQEQONISPLVERGPG 120
 QY 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 DB 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKDKQWQYIYKTSYDPDILLMKSARNSCWSDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKDKQWQYIYKTSYDPDILLMKSARNSCWSDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFFSVTVNEHLIDMDHEASFFGAFVVG 281
 DB 241 SIYGGIFELKENDRIFFSVTVNEHLIDMDHEASFFGAFVVG 281

RESULT 2

AAW27134 standard; protein; 281 AA.

AAW27134;

02-APR-1998 (first entry)

Human Apoptosis inducing molecule-I (AIM-I).

Apoptosis inducing molecule-I; AIM-I; autoimmune disorder;
 tumour necrosis factor ligand superfamily; AIM-I altered expression;
 neoplasia inhibition; anti-inflammatory agent.

Homo sapiens.

WO9733899-A1.

18-SEP-1997.

14-MAR-1996; 96WO-US003773.

14-MAR-1996; 96WO-US003773.

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM;

WPI; 1997-470807/43.

N-PSDB; AAT85210.

PT New isolated apoptosis inducing molecule-I - used to develop products for
 PT the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft
 PT versus host disease or inflammation.

PS Claim 2; Fig 1; 82pp; English.

CC The present sequence represents a human Apoptosis inducing molecule-I
 CC (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand
 CC superfamily. The products can be used in the diagnosis and treatment of
 CC disorders related to under-expression, over-expression or altered
 CC expression of AIM-I. AIM-I or agonists can be used for treating
 CC autoimmune disorders including systemic lupus erythematosus,
 CC immunoproliferative disease lymphadenopathy (ILD),
 CC angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis,
 CC diabetes, and multiple sclerosis, graft versus host disease, to inhibit
 CC neoplasia such as tumour cell growth, to treat restenosis, to regulate
 CC haematopoiesis in endothelial cell development, to stimulate peripheral
 CC tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be
 CC used for treating cachexia, cerebral malaria, rheumatoid arthritis or
 CC osteoporosis, for preventing graft-host rejection, and as anti-
 CC inflammatory agents, for treating endotoxin shock or to prevent
 CC activation of HIV

CC Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MAMMEVGGPSLIGQTCVLIVITFTVLLQSLCAVTVYVTFNKLKQMDKXSKGICFLKE 60
 QY 61 DSDYDNDDESMNSPCWQVQKQLRQVVKMLRTSEETISVQEQONISPLVERGPG 120
 DB 61 DSDYDNDDESMNSPCWQVQKQLRQVVKMLRTSEETISVQEQONISPLVERGPG 120
 QY 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 DB 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKDKQWQYIYKTSYDPDILLMKSARNSCWSDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKDKQWQYIYKTSYDPDILLMKSARNSCWSDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFFSVTVNEHLIDMDHEASFFGAFVVG 281
 DB 241 SIYGGIFELKENDRIFFSVTVNEHLIDMDHEASFFGAFVVG 281

RESULT 3

AAW19787 standard; protein; 281 AA.

AAW19787;

24-SEP-1997 (first entry)

Human apoptosis inducer cytokine TRAIL.

Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
 cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;
 thrombotic microangiopathy; therapy.

Homo sapiens.

Key Location/Qualifiers

FT Domain 1..18 /label= Cytolaemic_domain

FT Domain 19..38 /label= Transmembrane_domain

FT Domain 39..281

Query Match	100.0%	Score 1478	DB 2	Length 281
Best Local Similarity	100.0%	Pred. No. 2.6e-137		
Matches 281	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Sequence 281 AA				
Query	1	MAMMEVQGGPSIGQTCVLIIVFTVLLQSLCAVTVYVFTNELKQMDKYSKGIACFLKE	60	
Db	1	MAMMEVQGGPSIGQTCVLIIVFTVLLQSLCAVTVYVFTNELKQMDKYSKGIACFLKE	60	
QY	61	DDSYNDPDEBSMNSPCWQVVKQQLQVLRKMIILRSEETISTVDEKQONISPLVAERGPQ	120	
Db	61	DDSYNDPDEBSMNSPCWQVVKQQLQVLRKMIILRSEETISTVDEKQONISPLVAERGPQ	120	
QY	121	RVAAHITTRGRSNTLSSPNSKNEKALGRKXINSWSSRSGHSFLSNLIRNGELVIHEKG	180	
Db	121	RVAAHITTRGRSNTLSSPNSKNEKALGRKXINSWSSRSGHSFLSNLIRNGELVIHEKG	180	
QY	181	FYYIYSQCYFRFOEIKENTKNDKQWQYIYKYSYDPPIILMKSAARNSCWSKDAEYGLY	240	
Db	181	FYYIYSQCYFRFOEIKENTKNDKQWQYIYKYSYDPPIILMKSAARNSCWSKDAEYGLY	240	
QY	241	SIYGGIFELKENRIFVSVNNEHILMDHDAISFFGAFLVG	281	
Db	241	SIYGGIFELKENRIFVSVNNEHILMDHDAISFFGAFLVG	281	
RESULT 4				
ID	AAW76829	standard; protein; 281 AA.		
XC	AAW76829;			

XX	25-JAN-1999	(first entry)
DT	Human TL2 protein.	
XX		
XX	TR6; tumour necrosis factor related receptor; human; treatment; stroke;	
KM	inflammation; arthritis; septicæmia; autoimmune disease; restenosis;	
KM	transplant rejection; infection; ischaemia; brain injury; bone disease;	
KW	acute respiratory disease syndrome; acquired autoimmune disease syndrome;	
KW	AIDS; cancer; atherosclerosis; Alzheimers disease; TRALL; TNF;	
KM	TL2. tumour necrosis factor-related apoptosis-inducing ligand.	
XX		
OS	Homo sapiens.	
PN	EP870827-A2.	
XX		
PD	14-OCT-1998.	
XX		
PF	23-DEC-1997; 97EP-00310562.	
XX		
PR	14-MAR-1997; 97US-0041230P.	
PR	09-MAY-1997; 97US-00853684.	
XX		
PR	22-AUG-1997; 97US-00916625.	
XX		
PA	(SMK) SMITHKLINE BEECHAM CORP.	
PI		
XX	Deen KC, Young PR;	
XX		
DR	WPI: 1998-523156/45.	
XX		
DR	N-PSDB; AAV63096.	
XX		
PT	DNA encoding tumour necrosis factor receptor TR6 - and corresponding	
PT	polypeptide, antibody, agonist, antagonist, etc.	
XX		
PS	Disclosure; Page 32-33; 34pp; English.	
XX		
CC	This sequence represents the human tumour necrosis factor (TNF)-related	
CC	receptor, TL2 (also known as tumour necrosis factor-related apoptosis-	
CC	inducing ligand, TRALL). This protein is used in a method resulting in	
CC	the isolation of the novel human TNF related receptor, TR6. TR6	
CC	polypeptides and polynucleotides can be used in the treatment of chronic	
CC	and acute inflammation, arthritis, septicæmia, autoimmune diseases (e.g.	
CC	inflammatory bowel disease, psoriasis), transplant rejection, graft vs.	
CC	host disease, infection, stroke, ischaemia, acute respiratory disease	
CC	syndrome, restenosis, brain injury, (acquired autoimmune disease	
CC	syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative	
CC	disorders), atherosclerosis and Alzheimers disease	
XX		
SQ	Sequence 281 AA;	
XX		
Query Match	100.0%; Score 1478; DB 2; Length 281;	
Best Local Similarity	100.0%; Pred. No. 2.6e-137;	
Matches 281; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MAMMEVGGGDSIGOTCVLIVFTVLQSLCYAVTVYVFYFNEELKQMDPKYSKGIACFLKE 60	
DB	1 MAMMEVGGGPELIGOTCVLIVFTVLQSLCYAVTVYVFYFNEELKQMDPKYSKGIACFLKE 60	
QY	61 DDSYWDNDEDSNNSPCQYQYKQJRLVVRKMLITSEITISTVQEKQONISPLVRKGPQ 120	
DB	61 DDSYWDNDEDSNNSPCQYQYKQJRLVVRKMLITSEITISTVQEKQONISPLVRKGPQ 120	
QY	121 RVAHHITGTSRSTLSSPSNKKKALGRKINSMESRSRSHSFLSNLHNLNGELVTHKG 180	
DB	121 RVAHHITGTSRSTLSSPSNKKKALGRKINSMESRSRSHSFLSNLHNLNGELVTHKG 180	
QY	181 FYYIYSQTYRFRFOEIKENTKNDKQWQYIYKXTSYDPIILMKKSARNSCWSKDAEYGLV 240	
DB	181 FYYIYSQTYRFRFOEIKENTKNDKQWQYIYKXTSYDPIILMKKSARNSCWSKDAEYGLV 240	
QY	241 SIYGGIFELKENDRIFVSVTNHLIDMDHEASFPFGAFLVG 281	
DB	241 SIYGGIFELKENDRIFVSVTNHLIDMDHEASFPFGAFLVG 281	

RESULT 5
ID AAM56760 standard; protein; 281 AA.
XX AAM56760;
AC AAM56760;
XX 05-AUG-1998 (first entry)
XX
XX
DE Human TRAIL polypeptide.
XX
XX Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;
XX cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Domain 1..18 "N-terminal cytoplasmic domain"
FT /note="N-terminal cytoplasmic domain"
FT Region 19..38
FT /note="transmembrane region"
FT Domain 39..281
FT /note="extracellular domain"
XX
XX US763223-A.
XX
XX 09-JUN-1998.
XX
XX 25-JUN-1996; 96US-00670354.
XX
XX 29-JUN-1995; 95US-00496632.
XX 01-NOV-1995; 95US-00548368.
XX
XX (IMMUNEX CORP.
XX
XX Goodwin RG, Wiley SR;
XX
XX MPI; 1998-347322/30.
XX
XX N-PSDB; AAV29518.
XX
XX DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful
XX for producing recombinant polypeptides for research and therapy of
XX leukaemia, lymphoma, melanoma and viral infections.
XX
XX Claim 1; Col 33-36; 28pp; English.
XX
XX This represents a human tumour necrosis factor related apoptosis ligand
XX (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce
XX apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful
XX for producing the recombinant TRAIL polypeptides, which may be useful in
XX studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells
XX (e.g. to isolate antigens for vaccine development). The polypeptides can
XX be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal
XX treatment of blood or bone-marrow), or to treat viral infections
XX
XX Sequence 281 AA;
SQ
Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVAVYVFTNFKOMQDKYSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVAVYVFTNFKOMQDKYSGIACFLKE 60
QY 61 DDSTWMDNDESNMSPCMQVQKQRLQVLRKMLRTSEETISTVQEKQNIISPLVREKQPQ 120
DB 61 DDSTWMDNDESNMSPCMQVQKQRLQVLRKMLRTSEETISTVQEKQNIISPLVREKQPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWSSRSRGSFTLSNLTIRNGELVTHKKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWSSRSRGSFTLSNLTIRNGELVTHKKG 180

RESULT 6
ID AAM4354 standard; protein; 281 AA.
XX AAM4354;
AC AAM4354;
XX 28-MAY-1998 (first entry)
XX
XX
DE Human AGP-1.
XX
XX Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation;
XX bone resorption; haematopoietic disease.
XX
XX Homo sapiens.
XX
XX WO9746686-A2.
XX
XX 11-DEC-1997.
XX
XX 06-JUN-1997; 97MO-US009895.
XX
XX 07-JUN-1996; 96US-00660562.
XX
XX (AMGE-) AMGEN INC.
XX
XX Johnson MJ, Simonet WS, Denilenko DM;
XX
XX MPI; 1998-042194/04.
XX
XX N-PSDB; AAV15295.
XX
XX Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein -
XX useful for treating inflammation, bone resorption and haematopoietic
XX diseases.
XX
XX Claim 7; Page 36-37; 54pp; English.
XX
XX The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis
XX factor (TNF)-related protein, involved in inflammation, myelopoiesis and
XX bone resorption. It has the same nucleic acid and amino acid (aa)
XX sequences as the TNF-related apoptosis-induced ligand (TRAIL) described
XX in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay
XX reagents for detecting AGP-1 expression. Nucleic acid complementary to
XX AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are
XX used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus
XX erythematosus, psoriasis, scleroderma, infection-related inflammation) or
XX bone resorption diseases (e.g. osteoporosis, osteomyelitis,
XX hypercalcaemia, Paget's disease). AGP-1 can be used to treat
XX haematopoietic diseases associated with reduction in the number of bone
XX marrow cells, particularly neutrophils and lymphocytes, e.g. where caused
XX by disease, injury or exposure to myelosuppressive agents. Host cells,
XX transformed with expression vectors containing AGP-1 DNA, are used to
XX produce recombinant AGP-1
XX
XX Sequence 281 AA;
SQ
Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVAVYVFTNFKOMQDKYSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVAVYVFTNFKOMQDKYSGIACFLKE 60

QY 61 DDSYWDNDDESNMSPCWQVKMQLRQLVKMLIRTSEETISTVQEKQONISPLVREKGPQ 120
 Db 61 DDSYWDNDDESNMSPCWQVKMQLRQLVKMLIRTSEETISTVQEKQONISPLVREKGPQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVIEHKG 180
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVIEHKG 180
 QY 181 FYYIYSQTYFRFQBEIKENTKNDKQWQYIYKTSYDPDILMKSAANSCKSKDAEYGLY 240
 Db 181 FYYIYSQTYFRFQBEIKENTKNDKQWQYIYKTSYDPDILMKSAANSCKSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 281

RESULT 7
 AAY01517
 ID AAY01517 standard; peptide; 281 AA.
 AC AAY01517;
 DT 27-MAY-1999 (first entry)
 DE Protein associated with neurodegenerative and autoimmune diseases.
 DE Neurodegenerative disease; autoimmune disease; inflammatory disease;
 KM lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;
 KM surface receptor; TRAIL protein.
 OS Homo sapiens.
 OS FR2766713-A1.
 PN 05-FEB-1999.
 PD 04-AUG-1997; 97PR-00010176.
 PF 04-AUG-1997; 97PR-00010176.
 PR 04-AUG-1997; 97FR-00010176.
 XX (INMR) BIO MERIEUX.
 PA Rieger F, Belliveau JF, Perron H;
 PI MPI; 1999-156177/14.
 DR Use of polypeptide derived from TRAIL protein for diagnosis of
 XX PT degenerative disease - autoimmunity and inflammation, also useful in
 XX PT prevention or treatment, and similar use of corresponding ligand and
 XX PT nucleic acid.
 PS Claim 2, Page 13; 21pp; French.
 XX The specification describes the use a polypeptide corresponding to at
 CC least the primary sequence of part of the present sequence to produce a
 CC diagnostic, prophylactic or therapeutic composition useful in cases of
 CC degenerative, autoimmune and inflammatory diseases. The polypeptides can
 CC be used in treatment of neurodegenerative disease, lupus erythematosus,
 CC rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central
 CC nervous system cells, antigenic and specifically recognise the surface
 CC receptor of the TRAIL protein. The polypeptide is a marker of disease and
 CC a therapeutic target, e.g. its apoptotic activity can be blocked with an
 CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
 CC receptors, inhibiting formation of natural complex
 XX SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMNEVOGGPSLGGTCVLIVIFTVLQSLCVAVTYVFTNELKQMDKXSKGIACFLKE 60

Db 1 MAMNEVOGGPSLGGTCVLIVIFTVLQSLCVAVTYVFTNELKQMDKXSKGIACFLKE 60
 QY 61 DDSYWDNDDESNMSPCWQVKMQLRQLVKMLIRTSEETISTVQEKQONISPLVREKGPQ 120
 Db 61 DDSYWDNDDESNMSPCWQVKMQLRQLVKMLIRTSEETISTVQEKQONISPLVREKGPQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVIEHKG 180
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVIEHKG 180
 QY 181 FYYIYSQTYFRFQBEIKENTKNDKQWQYIYKTSYDPDILMKSAANSCKSKDAEYGLY 240
 Db 181 FYYIYSQTYFRFQBEIKENTKNDKQWQYIYKTSYDPDILMKSAANSCKSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 281

RESULT 8
 AAY27012
 ID AAY27012 standard; protein; 281 AA.
 AC AAY27012;
 DT 24-SEP-1999 (first entry)
 DE Human Apo-2 ligand (Apo-2L) polypeptide.
 DE Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
 KM lupus; immune-mediated glomerular nephritis; human.
 OS Homo sapiens.
 OS WO936535-A1.
 PN 22-JUL-1999.
 PD 15-JAN-1999; 99WO-US001039.
 PF 15-JAN-1998; 98US-00007886.
 PR 15-APR-1998; 98US-00060533.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Kelley RF, O'connel MT, Picti RM, Schwall RH;
 PI MPI; 1999-444397/37.
 DR N-PSDB; AAX86987.
 DR A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
 XX PT in mammalian cancer cells.
 XX Claim 1; Fig 1A; 86pp; English.
 XX This sequence represents a novel human cytokine, designated Apo-2 ligand
 CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
 CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
 CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
 CC induce apoptosis for pathological conditions characterized by decreased
 CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
 CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
 CC coding sequence can also be used in quantitative and screening diagnostic
 CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
 CC associated with increased apoptosis
 XX SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTGVLIIVFTVLLQSLCAVAVTVYVFTNELKMODKYSKGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTGVLIIVFTVLLQSLCAVAVTVYVFTNELKMODKYSKGIACFLKE 60
 QY 61 DDSTWDPNDESNMSPCMQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVERGQP 120
 DB 61 DDSTWDPNDESNMSPCMQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVERGQP 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSSGHSFLSNLHRNGELVTHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSSGHSFLSNLHRNGELVTHEKG 180
 QY 181 FYIYSQTYFFPFOEIKENTKNDKQWQYIYKYSYPPDILMKSRNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFFPFOEIKENTKNDKQWQYIYKYSYPPDILMKSRNSCWSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 9

AA81956
 ID AAY81956 standard; protein; 281 AA.

XX AAY81956;
 AC

XX 10-JUL-2000 (first entry)
 DT

XX Human Apo-2 ligand protein sequence.
 DE

XX Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;
 KW therapy; apoptosis; cancer.

XX Homo sapiens.
 OS

XX US6046048-A.
 XX

XX 04-APR-2000.
 PD

XX 08-JAN-1997; 97US-00780496.
 PF

XX 09-JAN-1996; 96US-0009755P.
 PR

XX (GETH) GENENTECH INC.
 PA

XX Kim KJ, Ashkenazi AJ, Chuntharapai A;
 PI

XX WPI; 2000-282690/24.
 DR

XX N-PSDB; AAA07425.
 DR

XX New isolated monoclonal antibodies having antigen specificity for Apo-2
 PT ligand, e.g. 2d6, 2E11 or 5C2, useful for detecting the expression of Apo-2
 PT -2 ligand serum, and for treating diseases associated with increased
 PT apoptosis.

XX Claim 9; Fig 1a; 46pp; English.
 PS

XX This sequence is the human Apo-2 ligand protein, which is recognised by
 CC monoclonal antibodies produced by the hybridoma cell lines of the
 CC invention. The hybridoma cell lines are deposited under the American Type
 CC Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258
 CC and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic
 CC assays for Apo-2 ligand, e.g. detecting its expression in specific cells,
 CC tissues, or serum. The antibodies may also be employed as therapeutics.
 CC For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand
 CC activity, like Apo-2 ligand-induced apoptosis, may be employed to treat
 CC pathological conditions or diseases associated with increased apoptosis.
 CC They are also useful for the affinity purification of Apo-2 ligand from
 CC recombinant cell culture or natural sources. The Apo-2 ligand itself may
 CC be used to treat diseases e.g. cancer, by inducing apoptosis in cells
 CC
 XX Sequence 281 AA;
 XX
 XX

Query Match 100.0%; Score 1478; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2,6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTGVLIIVFTVLLQSLCAVAVTVYVFTNELKMODKYSKGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTGVLIIVFTVLLQSLCAVAVTVYVFTNELKMODKYSKGIACFLKE 60
 QY 61 DDSTWDPNDESNMSPCMQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVERGQP 120
 DB 61 DDSTWDPNDESNMSPCMQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVERGQP 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSSGHSFLSNLHRNGELVTHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSSGHSFLSNLHRNGELVTHEKG 180
 QY 181 FYIYSQTYFFPFOEIKENTKNDKQWQYIYKYSYPPDILMKSRNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFFPFOEIKENTKNDKQWQYIYKYSYPPDILMKSRNSCWSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 10

AA824038
 ID AAB24038 standard; protein; 281 AA.

XX AAB24038;
 AC

XX 25-JAN-2001 (first entry)
 DT

XX Human PRO1096 protein sequence SEQ ID NO:51.
 DE

XX Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
 KW identification; tumourigenesis; anticancer; detection.

XX Homo sapiens.
 OS

XX WO200053750-A1.
 PN

XX 14-SEP-2000.
 PD

XX 02-DEC-1999; 99WO-US028551.
 PF

XX 08-MAR-1999; 99WO-US005028.
 PR

XX 01-SEP-1999; 99WO-US020111.
 PR

XX 29-OCT-1999; 99US-0162506P.
 PR

XX 30-NOV-1999; 99WO-US028313.
 PR

XX 01-DEC-1999; 99WO-US028634.
 PR

XX (GETH) GENENTECH INC.
 PA

XX Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;
 PI

XX WPI; 2000-594320/56.
 DR

XX N-PSDB; AAC58120.
 DR

XX Antibodies specific for PRO polypeptides, used to diagnose and inhibit
 PT the growth of tumors in mammals; and to identify inhibitors of PRO
 PT polypeptide activity or expression.

XX Claim 61; Fig 36; 226pp; English.
 PS

XX The present invention describes an antibody that binds to a human protein
 CC (I) selected from: PRO181; PRO1269; PRO1410; PRO1780; PRO3434;
 CC PRO1927; PRO3567; PRO1293; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397;
 CC PRO4407; PRO1555; PRO1096; PRO2038; and PRO2282. (I) has anticancer
 CC activity and can be used to diagnose tumours in mammals, by detecting
 CC complex formation when the antibody is contacted with test cells.
 CC Increased expression of genes encoding (I) can also be detected to

CC diagnose tumours. Agents which inhibit the activity of (1), especially
 CC the antibodies, or an antisense oligonucleotide which hybridises to genes
 CC encoding (1), can be used to inhibit tumour growth. Preferably by
 CC inducing cell death. Methods from the present invention can be used to
 CC identify compounds which inhibit the biological activity of (1). AAC58019
 CC to AAC58102 represent PCR primers and hybridisation probes used in
 CC examples from the present invention for human PRO sequences. AAC58103 to
 CC AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and
 CC protein sequences given in the exemplification of the present invention
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCAVATYVYFTNELKQMDKYSKGIACPLKE 60
 Db 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCAVATYVYFTNELKQMDKYSKGIACPLKE 60
 QY 61 DDSYMDPNDESNMSPCQWQKQRLQVVRKMLITSEITISTVOEKQNTSPLVREGRPQ 120
 Db 61 DDSYMDPNDESNMSPCQWQKQRLQVVRKMLITSEITISTVOEKQNTSPLVREGRPQ 120
 QY 121 RVAAHITGRGRNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLNGBELVYHEKG 180
 Db 121 RVAAHITGRGRNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLNGBELVYHEKG 180
 QY 181 FYTISQTYFRFOEIKENTKNDKQWQYTYKTSYDPDPLMKKSARNSCWSDAEYGLY 240
 Db 181 FYTISQTYFRFOEIKENTKNDKQWQYTYKTSYDPDPLMKKSARNSCWSDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFVWG 281
 Db 241 SIYGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFVWG 281

RESULT 11

AAB08545
 ID AAB08545 standard; protein; 281 AA.

AC AAB08545;

DT 20-DEC-2000 (first entry)

DE Amino acid sequence of a human TRAIL polypeptide.

XX Human; TRAIL; tumour necrosis factor; TNF; diterpenoid triepoxide;
 KW TNF related apoptosis-inducing ligand; tumour cell;
 KW TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma;
 KW non-small cell lung carcinoma.

OS Homo sapiens.

XX WO200048619-A1.

PD 24-AUG-2000.

PF 15-FEB-2000; 2000WO-US003891.

PR 16-FEB-1999; 99US-0120313P.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Rosen GD;

XX WPI; 2000-558253/51.

DR N-PSDB; AAA64325.

PT Killing of tumor cells, e.g. solid tumors or carcinoma, comprises
 PT administration of synergistic combination of diterpenoid diepoxide and
 PT tumor necrosis factor related apoptosis-inducing ligand.
 XX

ES Disclosure; Page 23-24; 23pp; English.

XX The present sequence represents a human TRAIL (tumour necrosis factor
 CC (TNF) related apoptosis-inducing ligand) polypeptide. The specification
 CC describes a method for enhanced killing of tumour cells. The method
 CC comprises contacting a susceptible tumour cell with a synergistic mixture
 CC of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined
 CC dosage to kill at least 50 % of the cells. This mixture is synergistic,
 CC and so is active at lower doses and against otherwise resistant cell
 CC lines. The method is used for killing tumour cells, especially solid
 CC tumours or carcinomas (especially mammary carcinoma or non-small cell
 CC lung carcinoma)
 XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCAVATYVYFTNELKQMDKYSKGIACPLKE 60
 Db 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCAVATYVYFTNELKQMDKYSKGIACPLKE 60
 QY 61 DDSYMDPNDESNMSPCQWQKQRLQVVRKMLITSEITISTVOEKQNTSPLVREGRPQ 120
 Db 61 DDSYMDPNDESNMSPCQWQKQRLQVVRKMLITSEITISTVOEKQNTSPLVREGRPQ 120
 QY 121 RVAAHITGRGRNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLNGBELVYHEKG 180
 Db 121 RVAAHITGRGRNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLNGBELVYHEKG 180
 QY 181 FYTISQTYFRFOEIKENTKNDKQWQYTYKTSYDPDPLMKKSARNSCWSDAEYGLY 240
 Db 181 FYTISQTYFRFOEIKENTKNDKQWQYTYKTSYDPDPLMKKSARNSCWSDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFVWG 281
 Db 241 SIYGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFVWG 281

RESULT 12

AAB28691
 ID AAB28691 standard; protein; 281 AA.

AC AAB28691;

DT 14-FEB-2001 (first entry)

DE Human AGP-1.

XX Human; AGP-1; type II transmembrane protein; cytosolic; antiviral;
 KW antiinflammatory; hepatotropic; arteriosclerotic; anti-HIV; HIV;
 KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;
 KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;
 KW transplant rejection; cardiovascular disease; arteriosclerosis.

OS Homo sapiens.

XX WO200063253-A1.

PD 26-OCT-2000.

PF 24-MAR-2000; 2000WO-US008004.

PR 16-APR-1999; 99US-00293245.

PA (AMGE-) AMGEN INC.

PI Hsu H, Meng S;

XX WPI; 2000-665240/64.

DR N-PSDB; AAC67831.

PT Fusion protein of AGP-1 protein and an Fc region, used to treat
 PT proliferative disorders, immune disorders, and virally-induced disorders.
 XX
 PS Claim 3; Fig 2; 93pp; English.

XX The present sequence is human AGP-1, a type II transmembrane protein.
 CC Fusion proteins comprising an Fc immunoglobulin region fused to the N-
 CC terminal portion of the AGP-1 protein have been produced. The fusion
 CC proteins can be used to induce apoptosis in a tissue, and to treat
 CC proliferative disorders, immune disorders, or virally-induced disorders.
 CC The proliferative disorders include cancers, such as breast, prostate,
 CC lung or colon cancer. The viral infections include hepatitis, and
 CC acquired immunodeficiency syndrome (AIDS), and the immune disorders may
 CC be autoimmune disorders or transplant rejection. Cardiovascular diseases
 CC such as arteriosclerosis may also be treated. The AGP-1 containing fusion
 CC proteins have increased biological activity compared to the soluble AGP-1
 CC proteins used in prior art therapies

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLQGTCLVIVFTVLLQSLCAVATVYVFTNELKQMDKXKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLQGTCLVIVFTVLLQSLCAVATVYVFTNELKQMDKXKSGIACFLKE 60
 QY 61 DDSYMDPNDSESMNSPCQWQVQWOLRQVLRKMLRTSEETISTVOEKQONISPLVRRGPQ 120
 DB 61 DDSYMDPNDSESMNSPCQWQVQWOLRQVLRKMLRTSEETISTVOEKQONISPLVRRGPQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLSNLHNLNGELVTHEKG 180
 DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLSNLHNLNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILLMKSAKNSCWDKAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILLMKSAKNSCWDKAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHASFQAFIVG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHASFQAFIVG 281

RESULT 13

AAB50977
 ID AAB50977 standard; protein; 281 AA.

XX AAB50977;
 DT 21-MAR-2001 (first entry)
 DE Human PRO1096 protein.

XX Human; PRO; cytostatic; neutropic; neuroprotective; respiratory general;
 KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
 KW PRO agonist; cancer; inflammatory disorder; immunological disorder.

XX Homo sapiens.

OS WO200073348-A2.

PN 07-DEC-2000.

PF 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-1999; 99WO-US012252.

PR 22-JUN-1999; 99US-0140650P.

PR 23-JUN-1999; 99US-0141037P.

PR 20-JUL-1999; 99US-0144758P.

PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.

PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028851.
 PR 09-DEC-1999; 99US-0170262P.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030999.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US005841.
 PR 02-MAR-2000; 2000US-0187202P.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.

XX (GENENTECH INC.

XX Baker RP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
 PI Shelton DL, Smith V, Watanabe CK, Wood WL;
 XX WPI, 2001-016509/02.

DR N-PSDB; AAC91579.

PT Twenty eight nucleic acids encoding PRO polypeptides which are useful for
 PT treating various tumors, e.g. breast cancer, and other inflammatory,
 PT angiogenic and immunological disorders.

PS Claim 31; Fig 54; 188pp; English.

XX The present sequence is of twenty eight novel PRO polypeptides. The
 CC PRO polypeptides and their agonists, including antibodies, peptides, and
 CC small molecule agonists, may be used to treat various tumors, e.g.,
 CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
 CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
 CC central nervous system cancer, melanoma or leukemia. They are also
 CC useful for treating other disorders such as neuronal, glial, astrocytal,
 CC hypochalamic and other glandular, macropnagal, epithelial, stromal and
 CC blastocelic disorders, and inflammatory, angiogenic and immunological
 CC disorders

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 4; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLQGTCLVIVFTVLLQSLCAVATVYVFTNELKQMDKXKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLQGTCLVIVFTVLLQSLCAVATVYVFTNELKQMDKXKSGIACFLKE 60
 QY 61 DDSYMDPNDSESMNSPCQWQVQWOLRQVLRKMLRTSEETISTVOEKQONISPLVRRGPQ 120
 DB 61 DDSYMDPNDSESMNSPCQWQVQWOLRQVLRKMLRTSEETISTVOEKQONISPLVRRGPQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLSNLHNLNGELVTHEKG 180
 DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLSNLHNLNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILLMKSAKNSCWDKAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILLMKSAKNSCWDKAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHASFQAFIVG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHASFQAFIVG 281

RESULT 14

AAB67243
 ID AAB67243 standard; protein; 281 AA.

XX	AAB67243;
AC	
DT	18-APR-2001 (first entry)
XX	
DE	Human Apo2 ligand.
XX	
KW	Human; Apo2 ligand: divalent metal ions; viral infection; cancer.
OS	Homo sapiens.
XX	
PN	WO200100932-A1.
XX	
PD	04-JAN-2001.
XX	
PF	26-JUN-2000; 2000WO-US017579.
XX	
PR	28-JUN-1999; 99US-0141342P.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;
PI	O'connell M, Pai R, Shahrokh Z, Simmons L;
XX	
DR	WPI; 2001-123012/13.
XX	
PT	Use of divalent metal ions for making Apo-2 ligand and in formulations
PT	containing Apo-2 ligand for increasing yield and stability of ligand
PT	trimers, useful for therapeutic applications.
XX	
PS	Claim 6; Fig 1; 60pp; English.
XX	
CC	The present invention relates to a formulation comprising Apo-2 ligand
CC	and divalent metal ions. Apo-2 ligand and the formulation are useful for
CC	treating cancers and viral infections. Addition of divalent metal ions
CC	for making Apo-2 ligand and formulations containing Apo-2 ligand results
CC	in increased yield and stability of Apo-2 ligand trimers
XX	
SQ	Sequence 281 AA;

OY 181 FYYISOTYFRPQBEIKENTKNDKMOYIYKYTSYPDPILIMKSARNSCMSKDAEYGLY 240
Db 181 FYYISQTYFRQBEIKENTKNDKMOYIYKYTSYPDPILIMKSARNSCMSKDAEYGLY 240
OY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

Search completed: September 5, 2004, 09:24:42
Job time : 73 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:26:17 ; Search time 73 Seconds
(without alignments)
1212.785 Million cell updates/sec

Title: US-10-662-431-2
Perfect score: 1478
Sequence: 1 MAMMEYCGSGSLQGTCTVIV.....NEHLIDMDHASFGLVWG 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues
Total number of hits satisfying chosen parameters: 1298764

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep.*
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 - 7: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep.*
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 - 18: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1478	100.0	281	8	US-08-916-625B-6
2	1478	100.0	281	8	US-08-971-317A-8
3	1478	100.0	281	9	US-09-813-329-17
4	1478	100.0	281	9	US-09-193-663-8
5	1478	100.0	281	9	US-09-934-465-1
6	1478	100.0	281	10	US-09-919-039-118
7	1478	100.0	281	12	US-10-202-062-20
8	1478	100.0	281	12	US-10-662-429-2
9	1478	100.0	281	12	US-10-662-430-2
10	1478	100.0	281	12	US-10-662-431-2
11	1478	100.0	281	12	US-10-652-244-2
12	1478	100.0	281	12	US-10-279-687-8
13	1478	100.0	281	13	US-10-039-785-66
14	1478	100.0	281	13	US-10-011-125-4
15	1478	100.0	281	13	US-10-001-054-54

16	1478	100.0	281	14	US-10-093-766-54	Sequence 54, Appl
17	1478	100.0	281	14	US-10-174-654-11	Sequence 11, Appl
18	1478	100.0	281	14	US-10-151-882-41	Sequence 41, Appl
19	1478	100.0	281	14	US-10-218-547-20	Sequence 20, Appl
20	1478	100.0	281	14	US-10-322-673-72	Sequence 72, Appl
21	1478	100.0	281	14	US-10-139-785-66	Sequence 66, Appl
22	1478	100.0	281	15	US-10-310-793-26	Sequence 26, Appl
23	1478	100.0	281	15	US-10-492-486-5	Sequence 5, Appl
24	1478	100.0	281	15	US-10-333-712-1	Sequence 1, Appl
25	1478	100.0	281	16	US-10-381-160-5	Sequence 13, Appl
26	1469	99.4	279	13	US-10-066-209-3	Sequence 3, Appl
27	1269.5	85.9	246	9	US-09-855-544A-13	Sequence 16, Appl
28	1017	68.8	208	9	US-09-855-544A-16	Sequence 11, Appl
29	988	66.8	253	12	US-10-652-244-11	Sequence 13, Appl
30	988	66.8	256	12	US-10-652-244-13	Sequence 6, Appl
31	985.5	66.7	461	12	US-10-652-244-13	Sequence 10, Appl
32	982	66.4	480	12	US-10-389-223A-6	Sequence 4, Appl
33	978	66.2	614	12	US-10-389-223A-2	Sequence 5, Appl
34	964.5	65.3	296	14	US-10-185-425-5	Sequence 14, Appl
35	937.5	63.4	188	9	US-09-855-544A-14	Sequence 6, Appl
36	930	62.9	291	10	US-09-873-829-6	Sequence 6, Appl
37	930	62.9	291	12	US-10-652-244-6	Sequence 6, Appl
38	930	62.9	291	13	US-10-017-910-6	Sequence 10, Appl
39	887	60.0	168	9	US-09-900-530A-10	Sequence 16, Appl
40	878	59.4	166	9	US-09-779-050A-16	Sequence 29, Appl
41	859	58.1	164	13	US-10-116-378-29	Sequence 11, Appl
42	850	57.5	161	14	US-10-216-074-7	Sequence 17, Appl
43	849	57.4	161	14	US-10-338-083-11	Sequence 15, Appl
44	636	43.0	172	9	US-09-779-050A-17	
45	561	38.0	113	9	US-09-855-544A-15	

ALIGNMENTS

RESULT 1
US-08-916-625B-6
Sequence 6, Application US/08916625B
Publication No. US20010010924A1
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH C.
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
TITLE OF INVENTION: RECEPTOR, TR6
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: RATHER & PRESTITA
STREET: P.O. BOX 980
CITY: VALLEY Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916, 625B
FILING DATE: 22-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/653, 684
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 60/041, 230
FILING DATE: 14-MARCH-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTITA, PAUL F
REGISTRATION NUMBER: 23, 031
REFERENCE/DOCKET NUMBER: GH-50008-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701

TELEX: 846169
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 281 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-916-625B-6

Query Match 100.0%; Score 1478; DB 8; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.2e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIVFTVLLQSLCVAVTYYVFTNELKQMDKXSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCVLIVFTVLLQSLCVAVTYYVFTNELKQMDKXSKSGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCQVQKQOLRQVAKMLRTSEETISTVOEKQONISPLVERGPQ 120
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 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
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 QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSAKNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSAKNSCWSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 2

US-08-971-317A-8

Sequence 8, Application US/08971317A
 Publication No. US20010010925A1

GENERAL INFORMATION:
 APPLICANT: Wiley, Steven R.
 TITLE OF INVENTION: TNF-DELTA LIGAND AND USBS
 TITLE OF INVENTION: THEREOF
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows
 SOFTWARE: FastSeq for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/971.317A
 FILING DATE: 17-NOV-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Goller, Mimi C
 REGISTRATION NUMBER: 39,046
 REFERENCE/DOCKET NUMBER: 6255, US.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (847) 935-7550
 TELEFAX: (847) 938-2623
 TELEX:
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:

LENGTH: 281 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. US20010010925A1
 US-08-971-317A-8

Query Match 100.0%; Score 1478; DB 8; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.2e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIVFTVLLQSLCVAVTYYVFTNELKQMDKXSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCVLIVFTVLLQSLCVAVTYYVFTNELKQMDKXSKSGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCQVQKQOLRQVAKMLRTSEETISTVOEKQONISPLVERGPQ 120
 DB 61 DDSYWDPNDEESMNSPCQVQKQOLRQVAKMLRTSEETISTVOEKQONISPLVERGPQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSAKNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSAKNSCWSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 3

US-09-813-329-17

Sequence 17, Application US/09813329
 Patent No. US20020012968A1

GENERAL INFORMATION:
 APPLICANT: Bristol-Myers Squibb Company
 TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Molec
 TITLE OF INVENTION: Variants Thereof
 FILE REFERENCE: D0016.np
 CURRENT APPLICATION NUMBER: US/09/813.329
 CURRENT FILING DATE: 2001-03-20
 PRIOR APPLICATION NUMBER: 60/190,816
 PRIOR FILING DATE: 2000-03-21
 NUMBER OF SEQ ID NOS: 65
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 17
 LENGTH: 281
 TYPE: PRT
 ORGANISM: Drosophila melanogaster
 US-09-813-329-17

Query Match 100.0%; Score 1478; DB 9; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.2e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIVFTVLLQSLCVAVTYYVFTNELKQMDKXSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCVLIVFTVLLQSLCVAVTYYVFTNELKQMDKXSKSGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCQVQKQOLRQVAKMLRTSEETISTVOEKQONISPLVERGPQ 120
 DB 61 DDSYWDPNDEESMNSPCQVQKQOLRQVAKMLRTSEETISTVOEKQONISPLVERGPQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSAKNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSAKNSCWSKDAEYGLY 240

QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVWG 281
 Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVWG 281

RESULT 4

US-09-193-663-8
 ; Sequence 8, Application US/09193663
 ; Patent No. US20020055624A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wiley, Steven R.
 ; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
 ; FILE REFERENCE: 6255.US.02
 ; CURRENT APPLICATION NUMBER: US/09/193,663
 ; PRIORITY FILING DATE: 1998-11-17
 ; EARLIER APPLICATION NUMBER: 60/065,916
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 281
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 US-09-193-663-8

Query Match 100.0%; Score 1478; DB 9; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.2e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIVIFTVLQSLCVAATVYVFTNELKQMDKXSGIACFLKE 60
 Db 1 MAMMEVGGPSLGGTCVLIVIFTVLQSLCVAATVYVFTNELKQMDKXSGIACFLKE 60
 QY 61 DDSYWDNDDESNMSPCWQVQKQRLQVVRKMLRTSEETISTVQEKQNIPLVRRGPQ 120
 Db 61 DDSYWDNDDESNMSPCWQVQKQRLQVVRKMLRTSEETISTVQEKQNIPLVRRGPQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHNRNGELVTHEKG 180
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHNRNGELVTHEKG 180
 QY 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSAKNSCWSKDAEYGLY 240
 Db 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSAKNSCWSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVWG 281
 Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVWG 281

RESULT 5

US-09-934-465-1
 ; Sequence 1, Application US/09934465
 ; Patent No. US20020102233A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; TITLE OF INVENTION: Apo-2 LIGAND
 ; FILE REFERENCE: 11669.22US03
 ; CURRENT APPLICATION NUMBER: US/09/934,465
 ; PRIORITY FILING DATE: 2001-08-21
 ; PRIOR APPLICATION NUMBER: 08/584,031
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patentln Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 281
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 US-09-934-465-1

Query Match 100.0%; Score 1478; DB 9; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.2e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIVIFTVLQSLCVAATVYVFTNELKQMDKXSGIACFLKE 60
 Db 1 MAMMEVGGPSLGGTCVLIVIFTVLQSLCVAATVYVFTNELKQMDKXSGIACFLKE 60
 QY 61 DDSYWDNDDESNMSPCWQVQKQRLQVVRKMLRTSEETISTVQEKQNIPLVRRGPQ 120
 Db 61 DDSYWDNDDESNMSPCWQVQKQRLQVVRKMLRTSEETISTVQEKQNIPLVRRGPQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHNRNGELVTHEKG 180
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHNRNGELVTHEKG 180
 QY 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSAKNSCWSKDAEYGLY 240
 Db 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSAKNSCWSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVWG 281
 Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVWG 281

RESULT 6

US-09-919-039-118
 ; Sequence 118, Application US/09919039
 ; Publication No. US20030108871A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kasear, Matthew R.
 ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
 ; FILE REFERENCE: PA-0035 US
 ; CURRENT APPLICATION NUMBER: US/09/919,039
 ; PRIORITY FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: 60/222,113
 ; NUMBER OF SEQ ID NOS: 401
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 118
 ; LENGTH: 281
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CD1
 US-09-919-039-118

Query Match 100.0%; Score 1478; DB 10; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.2e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIVIFTVLQSLCVAATVYVFTNELKQMDKXSGIACFLKE 60
 Db 1 MAMMEVGGPSLGGTCVLIVIFTVLQSLCVAATVYVFTNELKQMDKXSGIACFLKE 60
 QY 61 DDSYWDNDDESNMSPCWQVQKQRLQVVRKMLRTSEETISTVQEKQNIPLVRRGPQ 120
 Db 61 DDSYWDNDDESNMSPCWQVQKQRLQVVRKMLRTSEETISTVQEKQNIPLVRRGPQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHNRNGELVTHEKG 180
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHNRNGELVTHEKG 180
 QY 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSAKNSCWSKDAEYGLY 240
 Db 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSAKNSCWSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVWG 281
 Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVWG 281

RESULT 7
 US-10-202-062-20
 ; Sequence 20, Application US/10202062

Publication No. US20040038349A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.,
TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
FILE REFERENCE: PF559
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,838
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
LENGTH: 281
TYPE: PRT
ORGANISM: human
US-10-202-062-20

Query Match 100.0%; Score 1478; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVTVYVFTNELKQMDKSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVTVYVFTNELKQMDKSKSGIACFLKE 60
QY 61 DSYMDPNDDEESMNSPCWQVKWQLRQLVAKMLRTSEETISTVOEQQNIISPLVBERGPQ 120
DB 61 DSYMDPNDDEESMNSPCWQVKWQLRQLVAKMLRTSEETISTVOEQQNIISPLVBERGPQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVTHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVTHEKG 180
QY 181 FYIYSQTYFRQOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAAYGYL 240
DB 181 FYIYSQTYFRQOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAAYGYL 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 8
US-10-662-429-2
Sequence 2, Application US/10662429
Publication No. US20040038347A1
GENERAL INFORMATION:
APPLICANT: Ruben, Steven M
TITLE OF INVENTION: Apoptosis Inducing Molecule I
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/662,429
FILING DATE: 16-Sep-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/816,981
FILING DATE: 13-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kimball, Paul, C.
REGISTRATION NUMBER: 34,610
REFERENCE/DOCKET NUMBER: PF261

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-662-429-2

Query Match 100.0%; Score 1478; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVTVYVFTNELKQMDKSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVTVYVFTNELKQMDKSKSGIACFLKE 60
QY 61 DSYMDPNDDEESMNSPCWQVKWQLRQLVAKMLRTSEETISTVOEQQNIISPLVBERGPQ 120
DB 61 DSYMDPNDDEESMNSPCWQVKWQLRQLVAKMLRTSEETISTVOEQQNIISPLVBERGPQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVTHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVTHEKG 180
QY 181 FYIYSQTYFRQOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAAYGYL 240
DB 181 FYIYSQTYFRQOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAAYGYL 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 9
US-10-662-430-2
Sequence 2, Application US/10662430
Publication No. US20040048340A1
GENERAL INFORMATION:
APPLICANT: Ruben, Steven M
TITLE OF INVENTION: Apoptosis Inducing Molecule I
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/662,430
FILING DATE: 16-Sep-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/816,981
FILING DATE: 13-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kimball, Paul, C.
REGISTRATION NUMBER: 34,610
REFERENCE/DOCKET NUMBER: PF261
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 281 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-662-430-2

Query Match 100.0%; Score 1478; DB 12; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.2e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVLIYIFVLQSLCAVAVYVYFETNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCLVLIYIFVLQSLCAVAVYVYFETNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDPNDESNMSPCMQYKWLRLQVLRKMLRTSETTISTVQEKQNTSPVLRERGPQ 120
 DB 61 DDSYWDPNDESNMSPCMQYKWLRLQVLRKMLRTSETTISTVQEKQNTSPVLRERGPQ 120
 QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHFSNLHLNGLVTHEKG 180
 DB 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHFSNLHLNGLVTHEKG 180
 QY 181 FYIYISQTYRFPQEEIKENTKNDKQWQYLYKXTSPDPILMKKSARNSCWSKDAEYGLY 240
 DB 181 FYIYISQTYRFPQEEIKENTKNDKQWQYLYKXTSPDPILMKKSARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNHLLIDMDHEASFFGAFVLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNHLLIDMDHEASFFGAFVLVG 281

RESULT 10

US-10-662-431-2
 ; Sequence 2, Application US/10662431
 ; Publication No. US20040047864A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben, Steven M
 ; TITLE OF INVENTION: Apoptosis Inducing Molecule I
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/662,431
 ; FILING DATE: 16-Sep-2003
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/816,981
 ; FILING DATE: 13-MAR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kimball, Paul, C.
 ; REGISTRATION NUMBER: 34,610
 ; REFERENCE/DOCKET NUMBER: PF661
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 281 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-662-431-2

Query Match 100.0%; Score 1478; DB 12; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.2e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVLIYIFVLQSLCAVAVYVYFETNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCLVLIYIFVLQSLCAVAVYVYFETNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDPNDESNMSPCMQYKWLRLQVLRKMLRTSETTISTVQEKQNTSPVLRERGPQ 120
 DB 61 DDSYWDPNDESNMSPCMQYKWLRLQVLRKMLRTSETTISTVQEKQNTSPVLRERGPQ 120
 QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHFSNLHLNGLVTHEKG 180
 DB 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHFSNLHLNGLVTHEKG 180
 QY 181 FYIYISQTYRFPQEEIKENTKNDKQWQYLYKXTSPDPILMKKSARNSCWSKDAEYGLY 240
 DB 181 FYIYISQTYRFPQEEIKENTKNDKQWQYLYKXTSPDPILMKKSARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNHLLIDMDHEASFFGAFVLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNHLLIDMDHEASFFGAFVLVG 281

RESULT 11

US-10-652-244-2
 ; Sequence 2, Application US/10652244
 ; Publication No. US20040052788A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Godwin, Raymond G.
 ; TITLE OF INVENTION: Cyclokin that Induces Apoptosis
 ; FILE REFERENCE: 2835-E
 ; CURRENT APPLICATION NUMBER: US/10/652,244
 ; CURRENT FILING DATE: 2003-09-02
 ; PRIOR APPLICATION NUMBER: US/09/796,581
 ; PRIOR FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: 09/320,424
 ; PRIOR FILING DATE: 1999-05-26
 ; PRIOR APPLICATION NUMBER: 09/190,046
 ; PRIOR FILING DATE: 1998-11-10
 ; PRIOR APPLICATION NUMBER: 09/048,641
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 08/670,354
 ; PRIOR FILING DATE: 1996-06-25
 ; PRIOR APPLICATION NUMBER: 08/548,368
 ; PRIOR FILING DATE: 1995-11-01
 ; PRIOR APPLICATION NUMBER: 08/496,632
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 281
 ; TYPE: PRT
 ; ORGANISM: human
 ; US-10-652-244-2

Query Match 100.0%; Score 1478; DB 12; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.2e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVLIYIFVLQSLCAVAVYVYFETNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCLVLIYIFVLQSLCAVAVYVYFETNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDPNDESNMSPCMQYKWLRLQVLRKMLRTSETTISTVQEKQNTSPVLRERGPQ 120
 DB 61 DDSYWDPNDESNMSPCMQYKWLRLQVLRKMLRTSETTISTVQEKQNTSPVLRERGPQ 120
 QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHFSNLHLNGLVTHEKG 180

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Db      121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFTLSNHLNGBLVTHEKG 180
QY      181 FYIYISQTYRFRQBEIKENTKNDKQWQYIYKYTSYDPDILLMKASRNSCWSKDAEYGLY 240
Db      181 FYIYISQTYRFRQBEIKENTKNDKQWQYIYKYTSYDPDILLMKASRNSCWSKDAEYGLY 240
QY      241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLWG 281
Db      241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLWG 281

RESULT 12
US-10-279-687-8
; Sequence 8, Application US/10279687
; Publication No. US200302115099A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255, US.C2
; CURRENT FILING DATE: 2002-10-24
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 10/105,738
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/193,663
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/065,916
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-279-687-8

Query Match      100.0%; Score 1478; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAMMEVQGGPSIGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKXSKSGIACFLKE 60
Db      1 MAMMEVQGGPSIGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKXSKSGIACFLKE 60
QY      61 DSYWDPNDEESMNSPCQWQKQLRQIVRKMLRTSEETISTVQEKQONISPLVERGPQ 120
Db      61 DSYWDPNDEESMNSPCQWQKQLRQIVRKMLRTSEETISTVQEKQONISPLVERGPQ 120
QY      121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFTLSNHLNGBLVTHEKG 180
Db      121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFTLSNHLNGBLVTHEKG 180
QY      181 FYIYISQTYRFRQBEIKENTKNDKQWQYIYKYTSYDPDILLMKASRNSCWSKDAEYGLY 240
Db      181 FYIYISQTYRFRQBEIKENTKNDKQWQYIYKYTSYDPDILLMKASRNSCWSKDAEYGLY 240
QY      241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLWG 281
Db      241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLWG 281

RESULT 13
US-10-039-785-66
; Sequence 66, Application US/10039785
; Publication No. US20020067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunologically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07

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; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-785-66

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Db      61 DSYWDPNDEESMNSPCQWQKQLRQIVRKMLRTSEETISTVQEKQONISPLVERGPQ 120
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QY      181 FYIYISQTYRFRQBEIKENTKNDKQWQYIYKYTSYDPDILLMKASRNSCWSKDAEYGLY 240
Db      181 FYIYISQTYRFRQBEIKENTKNDKQWQYIYKYTSYDPDILLMKASRNSCWSKDAEYGLY 240
QY      241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLWG 281
Db      241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLWG 281

RESULT 14
US-10-011-125-4
; Sequence 4, Application US/1001125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-125-4

Query Match      100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 241 SIYQGGIFELKENDRIEVSVTNEHLIDMDEHASFPAFLVG 281
RESULT 15
US-10-001-054-54
; Sequence 54, Application US/10001054
; Publication No. US20020192209A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Baker, Kevin
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Hebert, Carolyn
; APPLICANT: Henzel, William
; APPLICANT: Kabakoff, Rhonda
; APPLICANT: Shelton, David
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITTING NEOPLASTIC
; FILE OF INVENTION: CELL GROWTH
; FILE REFERENCE: P3034R1PCT
; CURRENT APPLICATION NUMBER: US/10/001,054
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
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; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
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; PRIOR FILING DATE: 1998-04-24
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 PRIOR FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: PCT/US01/21735
 PRIOR FILING DATE: 2001-07-09
 PRIOR APPLICATION NUMBER: PCT/US01/27099
 PRIOR FILING DATE: 2001-08-29
 NUMBER OF SEQ ID NOS: 91
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 LENGTH: 281
 TYPE: PRT

ORGANISM: Homo Sapien
 US-10-001-054-54
 Query Match 100.0%; Score 1478; DB 13; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.2e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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